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4, 2006, 12:42:35; Search time 77.1431 Seconds (without alignments) 1378.343 Million cell updates/sec
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I IDGLRNIWIIKPAAKSRGRD.....IKVAVDRSCDIGNFELLWRQ 242
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj93360 Human BGS	Adj93365 Human tub	Human		Human		Adj93457 Human HOT	Abm80420 Tumour-as	Aab58909 Breast an	Abull512 Human MDD	Aau74334 Human cyt	Human	Human	Adj93455 Human HOT			Abb65541 Drosophil	Adq66614 Novel hum	Aam41236 Human pol		Abu00150 Human nov	Abb64074 Drosophil	Abb60840 Drosophil	Aam39105 Human pol
SUMMARIES	ID	ADJ93360	ADJ93365	ADJ93358	ADJ93366	AAB43005	AAM39450	ADJ93457	ABM80420	AAB58909	ABU11512	AAU74334	AAB94796	ADM05524	ADJ93455	ABB65645	ABU92048	ABB65541	ADQ66614	AAM41236	ABG05971	ABU00150	ABB64074	ABB60840	AAM39105
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* Query	Match	100.0	100.0	100.0	96.0	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.2	65.1	48.4	42.7	38.5	36.0	30.3	25.9	25.0	24.9	22.9	22.8
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Aam40891 Human pol Abp43750 Ligase TT Adj93458 Human tub Abb60296 Drosophil Adc31411 Human nov Adc31411 Human nov Adc31411 Human nov Adc31411 Human nov Adc31411 Human nov Adc31411 Human nov Adb55096 Drosophil Adj93373 Human BGS Adb65504 Human pro Abb22915 Protein # Adb65217 Human pro Abb64837 Drosophil Adj71954 Human pro Adb65217 Human mol Adj93456 Pig tubul Adm7968 Human mol Adm7968 Human nov Ade47756 Human Nov	ESULT 1 DJ93360 X ADJ93360 standard; protein; 242 AA. X ADJ93360 standard; protein; 242 AA. X ADJ93360 standard; protein; 242 AA. X ADJ93360 Y G-MAY-2004, (first entry) X Human BGS-42 protein sequence SeqID4. X testis-specific tubulin tyrosine-ligase-like polypeptide; X testis-specific tubulin tyrosine-ligase-like polypeptide; X Human BGS-42 protein sequence SeqID4. X testis-specific tubulin tyrosine-ligase-like polypeptide; X testis-specific tubulin tyrosine-ligase modulator; antiachbritic; antiachmatic; X netropycetetive; endocrine-Gen; antiachbritic; antiachmatic; X dematological; tyrosine ligase modulator; gene therapy; tubulin ligase; X dematological; tyrosine ligase modulator; proliferation; reproductive disorder; X meall intestine; brain; lymph tissue; infertility; Cushing's syndrome; X mozolo4005487-A2. X Homo sapiens. X Homo sapiens. X MOZO04005487-A2. X No-JUL-2002; 2002WG-0394725P. X 09-JUL-2002; 2002WG-0394725P.	<pre>ssine-ligase-like BGS-42 polypeptide, or ameliorating a medical condition, e.g reproductive disorders or testicular English.</pre>
AAM40891 ABP43750 AD593458 AB660296 ADC31066 ADC31411 ADC366481 ADC36681 ADC33373 ADB65204 AAM793373 ADB65217 ADH65217	ALIGNMENTS 242 AA. 242 AA. 242 AA. 11c; respirato 3en; antininfla tparkinsonian; unosuppressin, yase modulator 11ular cancer; proliferative proliferative proliferative proliferative n's disease; n's d	CO. CO. ing ion,
450477848744748884578	In; vence of the control of the con	SQUIBB On TC; bulin treat iferat
1304 423 983 321 321 483 673 873 1138 1138 1138 1103 377 377 377	standard; protein; 04. (first entry) -42 protein sequenc ecific tubulin tyro lypeptide; cytostat ecifor; endocrine-G ic; notropic; antipantipacterial; immi antipacterial; immi arboxypeptidase; cat r disorder; testicu. estinal disorder; cer; r disorder; cancer; r disorder; brain; lympi ; pneumonia; Addiso 's disease; immunol cer; liver cancer; ly preumonia; Addiso 's disease; immunol cer; sjogren's dise ens. 487-A2. 03; 2003WO-US021605	SS
σгго 4440 H υ α α α α α и и и и α α α	idard (firm (firm (firm (firm (firm)) (firm)	S, S, Self:
22 222 222 221 221 221 220 220 220 220 2	anda (f. 2 pr. 2 pr. 1	Nu S, N -099381/10 s-specific r preventi cellular p
25 295 296 295 296 295 5 298 295 5 298 24 5 298 24 8 24 8 24 8 24 9 24 9 24 9 24 9	RESULT 1 ADJ93360 ID ADJ93360; XX AC ADJ93360; XX XX ED Human BGS-42 XX	BRIM) BR eder JN, PI; 2004- ew testis seful for cerrant c isorders.
	RESU ADL90 ACX ACX ACX ACX ACX ACX ACX ACX ACX ACX	X X X X X X X Z X X X X X X X X X X X X

De useful 101 controlled to compounds with a cytocact, respiratory, antinflammatory, anabolic, hypertensive, endocrine-Gen, gastrointestinal-Gen, pypertensive, osteopathic, nootropic, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antinflammatory, antiseborrheic or derabological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BSS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition when as a disorder related to aberrant cubulin ligase activity, a disorder related to aberrant tubulin.

Carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsies, acromegaly, Alzheimer's disease, or Parkinson's disease or scleroderma. The BGS-42 polypeptides are the present sequence is that of the human to segment the BGS-42 protein (partial sequence) of the invention. This invention relates to a novel testis-specific tubulin tyrosine-ligase -like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory

Sequence 242 AA;

ö 180 120 61 TKFDIRQWFLVTDWNPLTIWFYKGSYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120 SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSWKKAIAHAMKVAQDHVEFRKNSFEL 180 240 181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLW 240 9 1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 1 idgirniwiikpaaksrgrdivcmdrveeilelaaadhpisrdnkwvvQKYIETPLLICD TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 0; Gaps Length 242; Indels ; Score 1299; DB 8; ; Pred. No. 1.9e-134; 0; Mismatches 0; 100.0%; Query Match Best Local Similarity 100. Matches 242; Conservative 241 RQ 242 242 S. 121 61 121 181 241 셤 8 d ð g ઠે g ઠે ò 셤

testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
Bustoprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
demaclogical; tyrosine ligase moddlator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer; Human tubulin tyrosine ligase protein consensus sequence SeqID13. ADJ93365 standard; protein; 541 AA. (first entry) 06-MAY-2004 ADJ93365; %&&&&&&&&&&&&&&

gastrointestinal disorder; colon cancer; stomach cancer; neural disorder; brain cancer; liver cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; parkinson's disease; immunological disorder; arthritis; asthma; AIDS; sepsis; acne; Sjogren's disease; scleroderma; human. New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular (BRIM) BRISTOL-MYERS SQUIBB CO. 09-JUL-2002; 2002US-0394725P. 09-JUL-2003; 2003WO-US021605. Nelson TC; WPI; 2004-099381/10. Wu S, N-PSDB; ADJ93364 WO2004005487-A2. Homo sapiens. 15-JAN-2004. Feder JN, Synthetic. disorders.

Example 4; SEQ ID NO 13; 343pp; English.

This invention relates to a novel testis-specific tubulin tyrosine-ligase

-like polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory,

den, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,

antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,

imminosuppressive, antiseborinteic or dermatological activity acting as

tyrosine ligase modulators. In addition, the disclosed sequences may be

useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be

useful for dagnosing a pathological condition or a susceptibility to a

pathological condition in a subject, and for preventing, treating or

meliorating a medical condition, such as a disorder related to aberrant

cubulin ligase activity, aberrant cellular proliferation, reproductive

carboxypeptidase activity, aberrant cellular proliferation, reproductive

disorders, testicular disorders, testicular cancer, pulmonary disorders,

lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,

neural disorders, brain cancer, liver concer, pulmonary disorders,

cueval for preptide can be used as a preventive agent for immunological

disorders including arthritis, asthma, AIDS, sepsies, acromegaly, Alahaimer's disease, or Parkinson's disease, or

disorders including arthritis, asthma, AIDS, sepsies, acromegaly, Alahaimer's disease, or Parkinson's disease or scleroderma. The antibodies may be used to purify, detect and

target the BGS-42 polypeptides. The present sequence is that of the

target the BGS-42 polypeptides. The present sequence is that of the

exemplification of the invention.

Sequence 541 AA;

Gaps ö 100.0%; Score 1299; DB 8; Length 541; Indels ; Pred. No. 6e-134; 0; Mismatches 0; 100.08; Matches 242; Conservative Similarity Query Match Best Local S

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252 193 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR

parnological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive configurates, testicular disorders, colon cancer, plumonary disorders, lung cancer, plumonary disorders, colon cancer, stomach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition configuration polymeptide, polymelectide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's collesse, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polymeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 protein of the invention.

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Sequence 541 AA;

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testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
antiantective; endocrine-Gen; antiantentitic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiathritic; antiasthmatic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation, reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; neural disorder;
brain cancer; liver cancer; proliferation; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
parkinson's disease; immunological disorder; arthma; AlDS;
                             312
                                                                      e.g.
                 SPLLPAHNWWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                     YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sepsis; acne; Sjogren's disease; scleroderma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; SEQ ID NO 2; 343pp; English.
                                                                                                                                                                                                                                                                                                      Human BGS-42 protein sequence SegID2
                                                                                                                                                                                                               ADJ93358 standard; protein; 541 AA.
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                                                                                                                                                                                                                                                                     06-MAY-2004 (first entry)
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N-PSDB; ADJ93357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alstheimer's disease;
Parkinson's disease; immunological disorder; arthritis; asthma; AlDS;
sepsis; acne; Sjogren's disease; scleroderma; human; TTL1 domain.
                                                                                   9
                                                                               1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD
                                                                                                       133 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                                                                          61 TKPDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                              193 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                    SPLLPAHNWTSTRFQEYLQRQGRGAVMGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                          253 SPLLPAHNMYTSTRFQEYLQRQGRGAVMGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                              181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLW
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     100.0%; Score 1299; DB 8; Length 541; 100.0%; Pred. No. 6e-134; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BGS-42 protein-related TTL1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ93366 standard; protein; 293 AA.
Query Match
Best Local Similarity 100.0
Matches 242; Conservative
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RQ 374
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This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial; immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be used for diagnosing a pathological condition or a susceptibility to a

08-FEB-2001 (first entry)

AAB43005;

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De userul for the development of compounds with a cytocatic, tespinatory cantinflammatory, anabolic, hypertensive, endocrine-Gen, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition, and so a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, colon cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, brain cancer liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymucleotide, or their modulators are also useful for treating infertility. Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromagaly, Alzhaimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthitis, asthma, AIDS, sepsis, acne, Sjogren's carget the BGS-42 polypeptides. The present sequence is that of the Tillity domain of the human BGS-42 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel testis-specific tubulin tyrosine-ligase -like polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory
                                                                                                                                                                                                                                                                                                                                 e.g.
                                                                                                                                                                                                                                                                                                  New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 14; 343pp; English
                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                    09-JUL-2002; 2002US-0394725P.
                                                  09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                   Wu S, Nelson TC;
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15-JAN-2004
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                                                                                          61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 120
                                                                                                                           TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120
                                                                                                                                          121 SPLLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180
                                                                        1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 60
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                               YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 233
                                               ;
                      Score 1247; DB 8; Length 293;
Pred. No. 1.4e-128;
                                               0; Indels
             96.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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Sequence 293 AA;
                                                233;
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AAB43005 standard; protein; 352 AA

RESULT 5
AAB43005
ID AAB4:

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiathritic; immunosuppressant; immunostimalant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; coaquences can be used for determining the presence of or predisposition cartivital; antithematic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be cused to treat cancers, proliferative disorders, neurodegenerative casoriated clasorders, osteoarthritis, graft vs host disease, cardiovascular disease, catorage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), ALDS, vital, bacterial or fungal infection, malaria, autoimmune cating damage, nocturnal haemcoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                  open reading frame; ORFX; detection; cytostatic; hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 850; DB 3; Length 352;
61.8%; Pred. No. 1.2e-84;
ive 41; Mismatches 49; Indels
                                                          Human ORFX ORF2769 polypeptide sequence SEQ ID NO:5538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 4720-4721; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127607P.
99US-0127636P.
99US-0127728P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2000; 2000US-00540763
                                                                                                                                                                                                                                                                                                       thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.8
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                     WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA,
                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000.
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous sinjuries, peripheral nervous and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral socierosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and part of the printed specification
 immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                               Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                  236
                                                                                                                                                                                              Wang D;
Zhao QA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CMS; Alzheimer's; Parkinson's disease; Humanington's disease; hamostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                              SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                               YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
        1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                               TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F, Wa
Zhang J,
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                        AAM39450 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-0048725.
25-APR-2000; 2000US-0052317.
20-UUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00520312.
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14-SEP-2000; 2000US-00662191.
0-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-0057344.
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                       ELLWRQ 242
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ELIYKQ 306
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BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory, anabolic; hypertensive;
osteopathic; nootropic; antipatkinsonian; antiarthritic; antiasthmatic;
anti-HV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; scomach cancer; neural disorder;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
sepsis; acne; Sjogren's disease; scleroderma; human; HOTTL3.
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                                                                                                                                                                                                                                                                                                          1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                                                                                YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                                                                            61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                  121 SPLLPAHNMWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                          Gaps
                                          4;
 65.4%; Score 850; DB 4; Length 352; 61.8%; Pred. No. 1.2e-84; ive 41; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HOTTL3 protein sequence SeqID2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ93457 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2003; 2003WO-US021605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                   Matches 152, Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            237 ELLWRQ 242
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ELIYKQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004005487-A2.
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                                                                                                                                                                                                                                                                                        181
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ABM80420 standard; protein; 352 AA.

ABM80420

(first entry)

18-NOV-2004

ABM80420;

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This invention relates to a novel testis-specific tubulin tyrosine-ligase completed designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory. Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiinflammatory, anabolic, hypertensive, activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptides activity. Semall intestine brain or lymph tissue. The BGS-42 polypeptide, polymucleotide, or their modulators are also useful for treating infertility. Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used a preventive agent for immunological disease a succepted the BGS-42 polypeptides. The present sequence is that of the human configurable. The present sequence does not appear in the specification but was obtained from
                                                                                                                                                                                                                                                e.9
                                                                                                                                                                                                               New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 7; 343pp; English.
                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
                    09-JUL-2002; 2002US-0394725P
                                                                                                                         Nelson TC;
                                                                                                                                                                     WPI; 2004-099381/10.
                                                                                                                         Wu S,
                                                                                                                         Feder JN,
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180
                                                                                                                                                                         YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF 236
                                                                                                                                                                                                                               241 YGADFVFGEDFOPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRMLDRNCDTGAF 300
                                                                                                        TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120
                                                     1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD
                                                                                                                                                            121 SPLLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                            Gaps
                            4,
 Length 352;
                            49; Indels
65.4%; Score 850; DB 8;
61.8%; Pred. No. 1.2e-84;
iive 41; Mismatches 49;
                            Conservative
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               Similarity
                           152;
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α RESULT

Sequence 352 AA;

Genbank

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and echods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies antagonists, binding molecules and compositions are useful concreased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, melanoma and leukaemia TAT nucleic acids may further be used as hybridisation probes, in ornowseeme and gene mapping, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120
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                                                                                                                 Tumour-associated antigenic target (TAT) polypeptide PRO80956, SEQ:1058
                                                                                                                                                        Tumour-associated antigenic target; TAT; human; overexpression; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system, melanoma and leukaemia. TAT nucleic acids may furthe used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention
                                                                                                                                                                           tumour, diagnosis, cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; badder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Indels
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61.8%; Pred. No. 1.2e-84;
iive 41; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO 1058; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002US-0414971P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate cancer or tumor.
                                                                                                                                                                                                                                                                                      gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-347921/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                       WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Best Local S
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YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF 236
                                                                                                 Breast and ovarian cancer associated antigen protein sequence SEQ ID 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                     nootropic, neurpprotective, antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuloer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autofimune thyroiditis; diabetes mellitus; Crobn's disease; multiple sclerosis; rhemmatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                        cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 1056-1057; 1299pp; English.
                                                                                                                                                                                                                                                                                                                       Human; breast cancer; ovarian cancer;
                                                                                                                                                                                                                      AAB58909 standard; protein; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                     ELLWRQ 242
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Sequences AAF21614 - AAF22011 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonists sequences exhibit cytostatic; immunosuppressive; nootropic; antiinflammatory; antiviral; antiallergic; hepatotropic; antidiabetic; untilingal; antiparasitic and cardiant activity. The polymucleotide and protein sequences are used in the diagnosis of cancer, particularly antients and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune

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          disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
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                                                                                                                                                                                                                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                              236
                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                         317
                                                                                                                                                                     1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; hillammation; osteoporosis; thrombocytopaenia;
 haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                            61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                         121 SPLLPAHNMWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                     YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chinn J;
                                                                                                                Length 362;
                                                                                                                                           Indels
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                                                                                                                                           49;
                                                                                                             65.4%; Score 850; DB 3;
61.8%; Pred. No. 1.3e-84;
iive 41; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU11512 standard; protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MDDT polypeptide SEQ ID 459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones AL, Tran AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2002; 2002WO-US009944.
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2001US-0280067P.
2001US-0280068P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2001; 2001US-0299776P.
20-JUN-2001; 2001US-0300001P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                        Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis; hepatitis.
                                                        infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                  237 ELLWRQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                    318 ELIYKQ 323
                                                                                                                          Similarity
                                                                                  Sequence 362 AA;
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29-MAR-2001;
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                                                                                                               Query Match
Best Local 8
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and hepatotropic activity. The polymucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma, anaemia, crohn's syndromes (ALDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABUI1450-ABUI1045 represent the MDDT polymucleotides encoded the sequence data for this patent did not form part of the invention. NoTE: The sequence data for this patent did not form part of the printed general part of the printed procession, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder;
cell proliferative disorder; inflammatory disorder; prion disease;
vesicle trafficking disorder; gastrointestinal disorder; muscle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 60
                                                                                                                                         New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yap PE, Amshey SR;
Kleefeld Y, Gerstin EH;
Panzer SR, Harris B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 850; DB 6; Length 399; Pred. No. 1.5e-84;
                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 459; 339pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Indels
Tuason O, Yap PE,
Nguyen DA, Kleefe
1, Chen AJ, Panzer
In RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytoskeleton-associated protein (CYSKP) #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
, Yu JY, Tuason
Liu TF, Nguyen
Lewis SA, Chen
Lo A, Lan RY, U
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 Hillman JL,
                 Daugherty SC, Dam TC,
Peralta CH, David MH,
Flores V, Marwaha R,
                                                                                               2003-058431/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                 N-PSDB; ABX34502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 399 AA;
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The invention relates to human cytoskeleton-associated polypeptides

C (CYSKP) and their associated polymuclectide sequences. The sequences are
useful in the treatment of disorders associated with overexpression or
underexpression of CYSKP in a patient. The disorders include cell

C underexpression of CYSKP in a patient. The disorders include cell

c underexpression of CYSKP in a patient. The disorders include cell

c arteriosclerosis, cirrhosis, hepatitis and psoriasis),

c autoimune/inflammatory disorders (such as, atherosclerosis,

c costeoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus

c and anaemia), vesicle trafficking disorders (such as

c disorderstinal disorders, prion diseases, neurological disorders (such

c as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,

thutington's disease, Parkinson's disease, amyotrophic lateral sclerosis

c and other motor neuron disorders), cell motility disorders, reproductive

cc disorders (such as endometriosis and polycystic ovary syndrome), muscle

disorders (such as myocarditis, migraine, hypertension, hypoglycaemia,

c disorders (such as myocarditis, migraine, dystrophy, spinal cord

diseases, central nervous system disorders (such as bown syndrome and

c rerebral palsy) and mental disorders (such as anxiety and schizophrenia).
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                                                                                                                                                                                                                                                                                                                                                  Hillman JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorder; cell motility disorder; reproductive disorder; spinal cord disease; central nervous system disorder; mental disorder; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cytoskeleton-associated proteins and polynucleotides, useful for diagnosing, preventing and treating cell proliferative, autoimmune, inflammatory, neurological, cell motility, reproductive and muscle
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Burford N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 850; DB 5;
61.8%; Pred. No. 2e-84;
ive 41; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                Lu DAM, Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 130-131; 194pp; English.
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                                                                                                                                                                                                                                     08-MAY-2000; 2000US-0202729P.
05-JUN-2000; 2000US-0209705P.
07-JUN-2000; 2000US-0210149P.
21-JUN-2000; 2000US-021315P.
                                                                                                                                                                                     03-MAY-2001; 2001WO-US014355
                                                                                                                                                                                                                                                                                                                                                                y YT, Au-Young J
Lal P, Yao MG,
                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                              Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS99894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 488 AA;
                                                                                                                WO200185942-A2.
                                                                             Homo sapiens.
                                                                                                                                                                                                                      05-MAY-2000;
                                                                                                                                                15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                 Azimzai Y,
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                     Saito K, Yamamoto J; , Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 15921; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                              Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                    Hayashi K,
                                                                                                                                                      Human protein sequence SEQ ID NO:15921
                                                                                               AAB94796 standard; protein; 744 AA
                                                                                                                                                                                                                                                                                                                                    Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                      27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                                                               99JP-00248036
                                                                                                                                   (first entry)
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ELIYKQ 306
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                                   ELLWRQ 242
                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                          EP1074617-A2.
                                                                                                                                   26-JUN-2001
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                 241
                                                                                                                 AAB94796;
181
                                   237
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                                                                                       AAB94796
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification, where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisents to the
complementary strand of a polynucleotide omprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotide which complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide comprises a 1'-end sequence, where the
complementary strand of a polynucleotide comprises a 1'-end sequence, where the combination of
complementary strand of a polynucleotide sand the complementary to a
coligonucleotide comprises at least 15 nucleotides and the combination of
coligonucleotide comprises at least 15 nucleotides and the combination of
coligonucleotide comprises at least 15 nucleotides and the combination of
coligonucleotide which comprises at least 15 nucleotides
coligonucleotide comprises at least 15 nucleotides
coligonucleotide comprises at least 15 nucleotides
coligonucleotide comprises at least 15 nucleotides
coligonucleotides
complementary to a primer sets can be used in antisense therapy and in
coligonucleotides. The primers allow obtaining of the full-length
coligonucleotides
complementary to the
complementary to a
complementary to complementary to complementary
coligonucleotides
coligonucleotides
complem
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Sequence 744 AA;

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120
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                                                                                                                                                                                                                                                                   236
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM6502-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM01378 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaccutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                 1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                                                                                                                                   393 HPLLPPDNWWSSQRRQAHLQEMGAPNAWSTIIVPGMKDAVIHALQTSQDTVQCRKASFEL
                                                                                                                                                                                                                                                                  YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                                                                61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                 121 SPLLPAHNMWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
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     Length 744;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; gene therapy; diagnostic marker; pharmaceutical.
                                  49;
Query Match
65.4%; Score 850; DB 4;
Best Local Similarity 61.8%; Pred. No. 3.7e-84;
Matches 152; Conservative 41; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein of the invention SEQ ID NO:4209.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM05524 standard; protein; 326 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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513 ELIYKQ 518
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                                                                                                                                                                                                                                                                                                                                 237 ELLWRQ 242
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Disclosure; SEQ ID NO 5; 343pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic,
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; neural disorder;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; luug;
emplysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; atthritis; asthma; AlDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g.
                                                                                                                     TKFDIROWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVOKYLKNDVGR 120
                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e aberrant cellular proliferation, reproductive disorders or testicular disorders.
                                                                                                                                                                                                                         1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD
                                                                                        SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                             YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                     Gaps
                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sepsis; acne; Sjogren's disease; scleroderma; human; HOTTL.
                               Length 326;
                                                     IndelB
                                                      49;
                               65.2%; Score 847; DB 7; 61.8%; Pred. No. 2.4e-84;
                                                      41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Human HOTTL protein sequence SegID2.
                                                                                                                                                                                                                                                                                                                                        ADJ93455 standard; protein; 292 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feder JN, Wu S, Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                      Conservative
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                                                                                                                                                                                                                                                          ELLWRQ 242
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ELIYKQ 306
                                           Local Similarity
nes 152; Conserv
           Sequence 326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004005487-A2
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                                 Query Match
                                            Best Loca
Matches
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cantinflammatory, anabolic, hypertensive, endocrine-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, denigate antiparthic, antiasthmatic, antiathmy, antibacterial, immunosuppressive, antistrhmitic, antiasthmatic, noctropic, antiparthinsonian, antisteborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition or a susceptibility to a meliorating a medical condition, such as a disorder related to aberrant tubulingase activity, a disorder related to aberrant tubuling carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidases activity, aberrant cellular proliferation, reproductive corboxypeptidases activity, aberrant cellular proliferation, reproductive carboxypeptidases activity, aberrant cellular proliferation, reproductive corporates, brain cancer, liver cancer, or proliferative condition cancer, agastrointestinal disorders, control and sisorders, brain cancer, or proliferative condition cancer treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alaheimer's disease, or Parkinson's disease. The BGS disease, or payeride can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's carget the BGS-42 polypeptides. The present sequence is that of the human corporate the BGS-42 polypeptides. The present sequence is that of the human corporation which is related to the invention but was obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is invention relates to a novel testis-specific tubulin tyrosine-ligase ke polypeptide. designated the BGS-42 polypeptide. The invention may useful for the development of compounds with a cytostatic, respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCHR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.1%; Score 846; DB 8; Length 292; 61.4%; Pred. No. 2.6e-84; ive 41; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 23727.
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Best Local Similarity
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ELIYKQ 246
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TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120 528 DKRLPSENMWDCYSFQAYLRQIGKYNMWLERIFPGMRKAIVGCMLASQENMDRRPNTFEL 587 121 SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD----IGNF 236 9 1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 7; Gaps 48.4%; Score 628.5; DB 4; Length 992; 48.4%; Pred. No. 1.6e-59; ive 50; Mismatches 70; Indels 7; Best Local Similarity 48.48 Matches 119; Conservative ELLWRQ 242 237 61 181 Query Match 요 셤 ઠ ઠ ઠે d ò ò

Search completed: April 4, 2006, 12:51:06 Job time: 78.1431 secs

|| :|| ELAYRQ 653

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12304, A 12358, A 12358, A 12473, App 2473, Appl 25, Appl 14, Appl 14, Appl 2871, Appl 2871, Appl 2871, Appl 2871, Appl 2871, Appl 27, App

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41 YFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEBILELAAADHPL 100
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                      US-11-087-099-12358
US-10-995-561-881
US-10-995-561-881
US-10-926-4608-0
US-11-072-512-2473
US-11-012-762-56
US-11-072-512-2408
US-11-167-831-9
US-11-167-831-9
US-11-167-831-9
US-11-167-831-9
US-11-167-831-1
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29.8%; Pred. No. 1.1e-18;
tive 43; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                              US-11-110-851-64
US-10-793-626-198
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US-11-096-274-2
US-11-203-806A-2
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TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: 084335-019
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 201-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-072-512-3371
; Sequence 3371, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKANATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.8
Matches 72; Conservative
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IRIE, RYOTARO
                                                                                                                      249
362
1047
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ORGANISM: Homo sapiens
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  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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Sequence 3658, Ap
Sequence 3621, Ap
Sequence 12196, A
Sequence 12195, A
Sequence 12194, A
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9522, Ap
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1: /SIDS5/ptodata/2/pubpaa/US08_NEW PUB.pep:*
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3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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5: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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61 IDGLR-----ADHPLSRDNK 105
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                                                         280 QYLASKHGPEAV--ETLFRDIDNIFVKSLQSVQKVIISDKHCFELYGYDILIDQDLKPWL 337
---TSPDYHPKKGCKWTLQRFR 279
                                  197 EYL-OROGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 DAAAPALEDL---PW-----PW----TSPGYLRPORVL--RMEEFFPETYRLD
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                                                                                                             256 IEINSSPTMHPSTPVTAQLCAQVQEDTIKV 285
                                                                                                                                    237 FAECLLWSGHRR-----QDVHLTNVAVQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US/350,978
PRIOR PELING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL full length CDNA
                                                                                                                                                                                                                                       Sequence 3621, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           : ISOGAI, TAKAO
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
                                                                                                                                                                                                                                                                                                                                                                                       ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYOTARO
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US-11-072-512-3621
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                HIO, YURI
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 VEVKDEGEWDFYWCDVSWLRENFDHTYMDEHVRISHFRNHYELTRKNYMVKNLKRFRKÓL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 EILELAAADHPLSRDNK------WVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWF 141
 DSAIHLCNNAVQK-----YLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVW---GS 210
                                                                                                                                  211 VIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSP--TMHPST 268
                                                                                                                                                         340 LLWKKIHRMVILTILAIAPSVPFAANCFELFGFDILIDDNLKPWLLEVNYSPALTLDCST 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --DLT-------QQYYSLVHGDAFISNSRNYFSQC 45
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                                                                              81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
ANGAHARI, KENJI
ASUHIKO
TITLE OF INVENTION: NOVel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US, 11/072, 512
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350, 978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEO ID NOS: 4096
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                   Sequence 3658, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUNKO
OTSUKA, KAORU
OTSUKA, KAORU
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LENGTH: 439
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APPLICANT:
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APPLICANT:
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
FILE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12194
    11;
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                                                                             88 EEILELAAADHPLSRDNKWVOKYIETPLLICDTKFD--IRQWFLVTDWNPLTIWFYKES 145
                                                                                                                                                                      198 YLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 RNLFRKCANLIERLKNSSPDSVNPRMILHALRELEMDSPKSSENEESGRLITPQEACNRI 419
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                                                                                                                                                                                                                                  146 YLRFSTORFSLDKLDSAIHLCNNAVQKY-LKNDVGR--SPLLPAHNMWTSTRFQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 RNYFSQCQALLARI----TSVNPQTDIDGLRNIWIIKPAA---KSRGRDIV---CMDRV
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    98; Indels
                                                                                                                                                                                                                                                                                                                                                                       ----EAEKOFLFEKIKLQDGHRPPQASS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 YLKRRLEEA-----EABKOPLFEKIKLQDGHRPPQASS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | NAME/KEY: misc_feature
| LOCATION: (1)..(596)
| PUTER INDEMATION: Ceres Seq. ID no. 15220178
| US-11-096-568A-12194
    46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 12194, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     258 INSSPTMHPSTPVTAQLCAQVQE 280
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; Sequence 5799, Application US/11087099
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    Conservative
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55;
  Matches
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                                                                          Sequence 12196, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
FURDING OF INVENTION:
FILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12196
LENGTH: 550
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12195
LENGTH: 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 YLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIE 257
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Pred. No. 0.43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1)...(550)
; OTHER INFORMATION: Ceres Seq. ID no. 15220180
US-11-096-568A-12196
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i_LCCATION: (1)..(579)
i_CTHER_INFORMATION: Ceres Seq. ID
US-11-096-568A-12195
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ORGANISM: Triticum aestivum
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Best Local Similarity
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US-11-096-568A-12195
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Sequence 879, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLOO1559
; CURRENT PILIOR DATE: 2004-11-24
; UNRENT FILIOR DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: PRACES (for Windows Version 4.0
; SEQ ID NO 879
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASESEQ for Windows Version 4.0
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359 -ATYLLLGRKSSELDASDSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRR 417
                                                                        199 LORQCRCAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEI 258
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                                                                                                                    Length 744;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.1%; Score 80; DB 6;
19.2%; Pred. No. 11;
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468 -ASPMLGNASNPNKADIPERKKSSTV 492
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                                                                                                                                                                                                               259 NSSPTM-HPSTPVTAQLCAQVQEDTI 283
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Matches 51, Conservative
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, ORGANISM: Homo sapiens
US-10-995-561-876
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US-10-995-561-876
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US-10-995-561-879
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Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CL001559

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1137;
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   Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
TITLE OF INVENTION: Genes and Uses for Plant CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.3%; Score 82; DB 7; Best Local Similarity 18.9%; Pred. No. 13; Matches 41; Conservative 39; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(1137)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-995-561-878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
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Matches
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Sequence 10927, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
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APPLICANT: Schable, Patrick S
APPLICANT: Ke, Jinshan
APPLICANT: Johnson, Jerry L
APPLICANT: Allred, Carolyn C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 A-----QVQEDTIKVAV 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wurtele, Eve S
Oliver, David J
Behal, Robert
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                                                                                                                                                                                                                                                                                       SEO ID NO 10927
LENGTH: 302
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US-11-167-856-26
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Publication No. US200502720541
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERBNCE: CLO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                        43 SQCQALLINRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEBILELAAADHPLSR 102
                                                                                                                                                                                 103 DNKWV------VQKYIETPLLICDTK------PDIRQWFLVTDWNPLTIWFY 142
                                                                                                                                                                                                                                                    143 KESYLRFSTQRFSLDKLDSA----IHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEY 198
                                                                                                                                                                                                                                                                                    382 -ATYLLLGRKSSELDASDSSSSNLSLAKVRPSSDLNNSTGOSPHHKVQRSVSSSQKORR 440
                                                                                                                                                                                                                                                                                                                       199 LORQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEI 258
                                                                                                                                                                                                                                                                                                                                              103 DNKWV------VQKYIETPLLICDTK------FDIRQWFLVTDWNPLTIWFY 142
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                                                                                                                                                  301 TDČENLIKKFLVLNP-----IK-----RĠ-----TLEQIMK-----
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                                                    DB 6; Length 752;
                                                                                  97; Indels
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                                           5.1%; Score ov,
19.2%; Pred. No. 12;
rive 42; Mismatches
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491 -ASPMLGNASNPNKADIPERKKSSTV 515
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468 -ASPMLGNASNPNKADIPERKKSSTV 492
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                                                                 Best Local Similarity 19.2 Matches 51; Conservative
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ORGANISM: Homo sapiens
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Matches 51; Conserv
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US-10-995-561-877
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US-10-995-561-877
                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ETPLLICDTKFDIR----QMPLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AVQKYLKND--VGR-----SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 AIAHAMKVAQDHVEPRKNSFELYG---ADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 --PHVLKHIQEYALRAHNTLNLQGCSRADFILRDDELLFLLEVNTIPGMSATSLVPREAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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APPLICANT: Wen, Tabi-Jung
APPLICANT: Wen, Tabi-Jung
TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Acetyl CoA Levels in Plants
FILE REPERBYCE: P2194USDIV-2
CURRENT APPLICATION NUMBER: US/11/167,856
CURRENT FILING DATE: 2005-06-27
APPLICANT: KADILY, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FORM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT PELING DATE: 2005-04-04
PRIOR PILING DATE: 2005-04-04
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FREESENCE: 14433
SOFTWARE: FREESENCE: 14433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 TCLDPLYDFDXIVEVAEKQDVA---FILLHGSPGEDGIL------QALLERVGCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 TSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TSADAVEDLTE----AEWEDLTQQYYSLVHG----DAFISNSRNYFSQCQALLNRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.1%; Score 79.5; DE Best Local Similarity 21.1%; Pred. No. 3.9; Matches 67; Conservative 53; Mismatches
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Sequence 25933, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

ITILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 DTKFDIRQWFLVTDWNPL----TIWFYKESYLR-----FSTQRFSLDKLDSAIHLCNNAV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 DAARSDRPRFAVGKYTAYDCSGLLWAPFEPYLRQARRICATELFSATRLESFEHIRDEEV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 RVMLRQLRQLAGR-----TVRLRDYLQMLALGVISRIVL---GKK---YVMEEA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 Q---KYLKNDVGRSPLLPAHNMISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 79; DB 7; Length 470; 26.1%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 QD-----HVEPRK-----NSFELYGADFVLGRDFRPWL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)._(470)
; OTHER INFORMATION: Ceres Seq. ID no. 13496424
US-11-096-568A-25993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: April 4, 2006, 12:59:34
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.14
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                          RESULT 15
US-11-096-568A-25993
                                                                                                                                                                                                                                                                                                       SEQ ID NO 25993
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-159220922
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 25994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 DTKFDIRQWFLVTDWNPL----TIWFYKESYLR----FSTQRFSLDKLDSAIHLCNNAV 170
                                                                                                                                                                                                                                                                                                                                                                                                                        104 NKWVVQKYIETPILLICDTKFDI -----RQWFLVTDWN-PLTIWFYKESYLRFSTQRFSLD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | | : | : | : : : | | : : : PLIGAIAAGNIVLLK-----SSELSPNASAFLAKTIPAYLDTKAIKVIEGGPDVATIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----WGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYG-----ADFVL-GRDFRPWLIE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 Q---KYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVA 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Gaps
                                                                                                                                                                                                                                                                                                                                                                               51; Gaps
                                                                                                                                                                                                                                                                                                                            Query Match 5.1%; Score 79.5; DB 7; Length 433; Best Local Similarity 22.5%; Pred. No. 6.3; Matches 42; Conservative 25; Mismatches 69; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.1%; Score 79; DB 7; Length 462; Best Local Similarity 26.1%; Pred. No. 7.6; Matches 42; Conservative 23; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 QD-----HVEPRK-----NSFELYGADFVLGRDFRPWL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 ADGEGDSAPAITPAEFREMVDEFFALHGA-FNIG-DYIFWL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
| LOCATION: (1).7(462)
| OTHER INDEMATION: Ceres Seq. ID no. 13496425
| US-11-096-568A-25994
PRIOR APPLICATION NUMBER: US 10/293,865
PRIOR FILING DATE: 2002-11-13
PRIOR PPLICATION NUMBER: US 09/344,882
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Ver: 3.1
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis Thaliana
US-11-167-856-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 RVMLRQLRQAAGR-----
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US-11-096-568A-25994
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REPERBUCE: DO283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US. 60/394,725
PRIOR FILING DATE: 2002-07-09
                                   Sequence 21, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 38213, A
Sequence 3371, Ap
Sequence 21303, A
Sequence 262294,
Sequence 3658, Ap
Sequence 6, Appli
                                                                                                                                                                                                                                                  Sequence 118, App
Sequence 1, Appli
Sequence 12744, A
Sequence 2495, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKPDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLLPAHNMWISTRRQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLLPAHNWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 293
                      Sequence
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                               US-10-615-659-21
US-10-615-659-22
US-10-615-659-22
US-10-635-977-22
US-10-635-977-22
US-10-104-047-3371
US-10-104-047-3371
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US-10-104-047-3658
US-10-210-131-118
US-10-210-131-118
US-11-250-613-1
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Pred. No. 2.7e-151;
; Mismatches 0;
 US-10-635-977-8
US-10-424-599-205823
                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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Publication No. US20040157234A1
GENERAL INFORMATION:
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US-10-635-977-14
Sequence 14, Application US/10635977
; Publication No. US20040171131A1
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Best Local Similarity 100.0%; Po
Matches 293; Conservative 0;
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SOFTWARE: PatentIn version 3.2
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-615-659-14
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LENGTH: 293
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Sequence 14, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 13, Appl
Sequence 13, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
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617, App
617, App
5, Appli
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23415, A
36330, A
19014, A
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5, Appli
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5184, Ap
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26, Appl
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8, Appli
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2900.544 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                    April 4, 2006, 12:55:16; Search time 42.2072 Seconds
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-615-659-2
US-10-615-659-2
US-10-615-659-13
US-10-635-977-13
US-10-635-977-13
US-10-635-977-4
US-10-635-977-4
US-10-635-977-4
US-10-635-977-4
US-10-635-977-7
US-10-108-260A-4209
US-10-756-149-5267
US-10-108-260A-4209
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US-10-108-260A-4209
US-10-108-260A-4209
US-11-097-143-319014
US-11-097-143-3184
US-11-097-143-7680
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                                                                                                                                                                                                                                                                                                                 1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
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1560
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seq length: 200000000
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120 120 180 180 240 240

293

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; Sequence 13, Application US/10615659; Sequence 13, Application US/10615659; Publication No. US20040157234A1; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company; TITLE OF INVENTION: TYROSINE-LIGESELIKE PROTEIN, BGS42; TITLE OF INVENTION: TYROSINE-LIGESE-LIKE PROTEIN, BGS42; TITLE OF INVENTION WINDER: US/10/615,659; CURRENT APPLICATION NUMBER: US. 60/394,725; PRIOR APPLICATION NUMBER: US. 60/394,725; PRIOR FILING DATE: 2002-07-09; NUMBER OF SEQ ID NOS: 102; SOFTWARE: Patentin version 3.2; SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10635977

Publication No. US20040171131A1

REBERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: DO283A CIP

CURRENT APPLICATION NUMBER: US/10/635,977
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                    253 SPLLPAHNWTSTRFQEYLQRQCRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 312
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                                                                                 TKFDIROWFLVTDWNDLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVQKYLKNDVGR
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100.0%; Pred. No. 6.3e-151;
iive 0; Mismatches 0;
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Matches 293; Conservative
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ORGANISM: Homo sapiens
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US-10-615-659-13
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      APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: DOSBAS CIP
CURRENT APPLICATION NUMBER: US/10/635,977
CURRENT PILING DATE: 2003-08-07
RIOR PILING DATE: 2002-07-09
PRIOR PILING DATE: 2002-07-09
PRIOR PILING DATE: 2003-07-09
NUMBER: OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
LENGTH: 293
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Sequence 2, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILLE REFERENCE: D02083 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.2
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100.0%; Pred. No. 2.7e-151;
rative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 293; Conservative
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US-10-615-659-2
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US-10-635-977-14
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-10-615-659-2
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LENGTH: 541
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Sequence 4, Application US/10635977
; Sequence 4, Application WS/10635977
; Publication No. US2004017131A1
; GENERAL INFORMATION:
; APPLICANT: BISIGOL-MyETS SQUIBD COMPANY
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
; FILE REPERENCE: DO283A CIP
; CURRENT APPLICATION NUMBER: US. 10/635,977
; CURRENT APPLICATION NUMBER: U.S. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR PELLING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 103
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: DOL283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
FRICH REPLICATION NUMBER: U.S. 60/394,725
FRICH RILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 242
                                                                                                                                      253 SPLEPAHNWYSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 312
                 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVOKYLKNDVGR
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Best Local Similarity 100.0%; Pred. No. 2.8e-119;
Matches 233; Conservative 0; Mismatches 0;
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Publication No. US20040171131A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

CURRENT APPLICATION NUMBER: US/10/635,977

CURRENT FILING DATE: 2003-08-07

PRIOR FILING DATE: 2002-07-09

PRIOR FILING DATE: 2003-09-09

NUMBER OF SEQ ID NOS: 103

SOFTWARE: PATENTIAN OF SEQ ID NOS: 103

SEQ ID NO 13

LENGTH: 541
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                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                            100.0%; Score 1560; DB 4;
100.0%; Pred. No. 6.3e-151;
cive 0; Mismatches 0;
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: U.S.10/615,659
PRIOR PILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn version 3.2
LENGTH: 541
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 293; Conservative
                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-10-635-977-2
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; Publication No. US20040157234A1
; GENERAL INFORMATION:
    TELLE INFORMATION:
    APPLICANT: Bristol-Myers Squibb Company
    APPLICANT: Bristol-Myers Squibb Company
    TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
    TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
    TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
    FILE REFERENCE: D0283 NP
    FILE REFERENCE: 2003-07-09
    PRIOR APPLICATION NUMBER: U.S. 60/394,725
    PRIOR FILING DATE: 2002-07-09
    NUMBER OF SEQ ID NOS: 102
    SOFTWARE: Patentin version 3.2
    SEQ ID NO 7.
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                                                                                                  Query Match 79.9%; Score 1247; DB 4; L Best Local Similarity 100.0%; Pred. No. 2.8e-119; Matches 233; Conservative 0; Mismatches 0;
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Best Local Similarity 56.7%; Pred. No. 3.1e-84;
Matches 165; Conservative 48; Mismatches 78
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-615-659-7
                                                ; OKGANISH. ...
US-10-635-977-4
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RESULT 10

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Sequence 5267, Application US/10756149

Publication No. US20050181375A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A212, Natasha
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER,
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 5267
LENGTH: 352
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Best Local Similarity 56.7%
Matches 165; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 165; Conserv
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181 181 241

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62 EGDRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
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; Publication No. US20020039764A1
; GENERAL INPORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR APPLICATION NUMBER: 60/124,270
; RIGHER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 326;
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56.7%; Pred. No. 5.7e-84;
ive 48; Mismatches 78; Indels
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Publication No. US20040005560A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
APPLICANT: HELLY RESEARCH INSTITUTE
TILLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILLE REPERENCE: H1-A01106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATEUTIN Ver. 2.1
SEQ ID NO 4209
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Best Local Similarity 56.7°
Matches 165, Conservative
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; ORGANISM: Homo E
US-10-108-260A-4209
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US-10-108-260A-4209
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US-09-925-298-617
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                                                                     KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS 181
                                                                                                                                                              PLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY 241
                                                                                                                                                                                                                                                              DGLRNIWIIKPAAKSRGRDIVCMDRVBEILELAAADHPLSRDNKWVVQKYIETPLLICDT 121
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                                             DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDT
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APPLICANT: POLICKY, Jennifer L.
FITLE OP INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
FILE REFERENCE: PF-0772 USN
CURRENT APPLICATION NUMBER: US/10/275,595A
CURRENT APPLICATION NUMBER: US 60/201,960
PRIOR APPLICATION NUMBER: US 60/201,960
PRIOR FILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-06-08
PRIOR PRILING DATE: 2000-06-06
PRIOR PRILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
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OTHER INFORMATION: Incyte ID No: 2156553CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10275595A Publication No. US20040078804A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Dyung Aina M.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: AZIMZAI, Yalda
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YAO, Monique G.
BANDMAN, Olga
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Matches 165; Conservative
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ORGANISM: Homo sapiens
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US-10-275-595A-5
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Search completed: April 4, 2006, 12:58:00 Job time : 43.2072 secs
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                                                                        ORGANISM: Homo sapiens FEATURE:
NAME/KEY: SITE
LOCATION: (307)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-102-806-617
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                                                                                                                                                                                                                                                                            13 LTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKP
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Publication No. US20030054421A1

GENERAL INFORMATION:

APPLICATY: ROSE et al.

TILE OF INVENTION:

PILE REFERENCE: PA103P1C1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR APPLICATION NUMBER: 09/925,298

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR FILING DATE: 2000-03-08

SRIOL DATE: 1999-03-12

NUMBER OF SEC ID NOS: 846

SEC ID NO 617
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                                                                                                                                                                                                   57.5%; Score 897; DB 3; Length 362; 57.5%; Pred. No. 4.4e-83; tive 47; Mismatches 72; Indels
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 617
LENGTH: 362
TYPE: PRT
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Matches 161, Conservative
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LOCATION: (307)
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210 QRFQAHLQEMGAPNAWSTIIVPGMKDAVIHALQTSQDTVQCRKASFELYGADFVFGEDFQ 269
90 GAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWFLVT 149
                                                                                                                                                                                                                                             193 TRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFR 252
                                                                                                                                           150 DWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCHRHPLLPPDNMWSS
                                                                                                            DWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTS
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Run on:

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Sequence 4, Appli
Sequence 24306, A
Sequence 22, Appl
Sequence 31, Appli
Sequence 31126, A
Sequence 156, Appli
Sequence 156, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 16454, A
Sequence 16454, A
Sequence 2578, Appli
Sequence 26, Appli
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           Sequence
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; Sequence 3371, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX ESEBARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; TITLE OF INVENTION: NO. 6943241e1 full length cDNA
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR PAPLICATION NUMBER:
; RIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3371
US-09-134-001C-4588
US-09-075-375F-4
US-09-232-468A-22
US-09-784-984B-53
US-10-138-075-4
US-09-282-994A-33126
US-09-538-092-156
US-09-504-318-6
US-09-504-318-6
US-09-954-314-6
US-09-248-796-165
US-09-248-796-165
US-09-248-796-165
US-09-375-413A-12
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US-10-293-865-26
US-08-776-900C-23
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US-10-104-047-3658
Sequence 3658, Application US/10104047
Parent No. 6942241
GENERAL INFORMATION:
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     TYPE: PRT; ORGANISM: Homo sapiens
US-10-104-047-3371
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  Query Match
Best Local S:
Matches 72,
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Patent No. 5208144 -
Sequence 13504, A
Sequence 33, Appl
Sequence 6, Appli
Sequence 4, Appli
                                                                                                                                                                               4, 2006, 12:46:06; Search time 11.4368 Seconds (without alignments) 2118.072 Million cell updates/sec
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                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PeTuS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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; ORGANISM: Drosophila melanogaster
US-09-270-767-62411
                                                                                                           173 PLDTKVKSCLMADLL 187
                                                                                    269 PVTAQLCAQVQEDTI 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-104-047-3621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 HLCNNAVOKYLKN-----DVGRSPLLPAHNMWTSTRFQEYLQRQG---RGAVWG- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 QYLASKHGPEAV--ETLPRDIDNIFVKSLQSVQKVIISDKHCFELYGYDILIDQDLKPWL 337
                                                                                                                                                                                                                                                                                                                                                                 65 VEVKDEGEWDFYWCDVSWLRENFDHTYMDEHVRISHFRNHYELTRKNYMVKNLKRFRKQL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 YKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHN-----MWTSTRFQ 196
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                Length 439;
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                                                                                                                                                                                                                                                             ; Score 256.5; DB 2; Length '; Pred. No. 8.9e-20; 56; Mismatches 109; Indels
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-ADIOS
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3658
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                                                                                                                                                                                                                                                                16.4%;
25.5%;
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Best Local Similarity 25.5%
Matches 84; Conservative
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CORGANISM: Homo sapiens
US-10-104-047-3658
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Best Local Similarity
Matches 57; Conserv
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LENGTH: 561
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US-09-270-767-62411
; Sequence 62411, Application US/09270767
; Sequence 62411, Application US/09270767
; Fatent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: FILE Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT PILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 62411
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                                                                                                                                                                                                                                                      Sequence 3(21), Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA; FILE REFERENCE: H1-A0105
; CURRENT FILING DATE: 2002-03-25
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 4096
; NUMBER OF SEQ ID NOS: 4096
; SOFFWARE: PatentIN Ver. 2.1
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                                                                                                                                                                                                                                                                                              157 ---- DKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWISTRFQEYLQRQGRGAVWGSVI 212
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SERVERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Giot, Loic

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1990-04-01

PRIOR PLILING DATE: 2000-03-29;

PRIOR PLILING DATE: 2000-02-20;

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 31
                                                                                                                                                155 ----SLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQ--EYLQRQGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594 LDPYAYSVTDLKDLECHLTNTCLQS-KKKDKDSSVL------EPDSIEEIPNERKS
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                                                                                                                                                                                                                                                                                                                                                                                                                   213 YPSM----KKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSP
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                                                                             50;
                                  Length 259;
                                                                             81; Indels
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OTHER INFORMATION: Polypeptide Accession Number YBR094W
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21.8%; Pred. No. 7.2e-07;
tive 44; Mismatches 105;
                                                                                                                    60 DIDGLRNIWIIKPAAKSRGRDI----VCMDRVEEIL----
                                Query Match 9.7%; Score 151; DB 2; Best Local Similarity 22.6%; Pred. No. 2.6e-08; Matches 53; Conservative 50; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 PSTPVTAQLCAQVQEDTIKVAV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.89
Matches 57; Conservative
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US-09-538-092-31
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Sequence 14603, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: ROR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                    3;
                                                                                       53 TSVNPQTDI------DGLRNIWIIKPAAKSRGRDIVCMDRVEEILBLAAADHPL 100
                                                                                                                       101 SRDNKWVVQKYIETPLLIC-----DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 TSVNPQTDI------DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPL 100
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Sequence 46787, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOGTWARE: PatentIn Ver. 2.0

SEQ ID NO 46787

TYPE: PRT
                                                    Gaps
                                                    25;
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         Length 260;
                                                    43; Indels
Query Match 9.9%; Score 154.5; DB 2; Best Local Similarity 31.7%; Pred. No. 1.1e-08; Matches 40; Conservative 18; Mismatches 43;
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US-09-270-767-46787
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249 TLDHFD 254
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LENGTH: 259
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US-09-902-540-12305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 NNAVOKYLKNDVGRSPLLPA-----HNWW---TSTRFQEYLQRQGR--GAVWGSVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 ----UDKYIVGD----DYLPTWEVPSLRKYYNRFGGSMRTVFEAYVRDQGKDPAQIWPQVE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VÕEFVQRPYLVDGHKFDIGVYVVITSVNPLRVYIYTGDVLFRYCPVKYHPFDAEN---- 55
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclea acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nuclea acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DARE: 199-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                    GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 Y-----PSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTM 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : | | : : : | | : | : | 109 HIVRTTIAAKEKDIVNILRSYRTH-----NFFDLMRFDLFIDEDLKVFLMEANMSPNL 161
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.5%; Score 102; DB 2; Best Local Similarity 43.8%; Pred. No. 0.00073; Matches 21; Conservative 10; Mismatches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.1%; Score 126; DB 2;
Best Local Similarity 23.6%; Pred. No. 2.1e-05;
Matches 42; Conservative 36; Mismatches 62.
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; Sequence 12305, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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                       Sequence 46577, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-62317
                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Drosophila melanogaster US-09-270-767-46577
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US-09-270-767-62317
-09-270-767-46577
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LENGTH: 305
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LENGTH: 55
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53 TSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 LTIWFYKESYLRFSTORF-SLDKLDSAIHLCN--NAVQKYLKNDVGRSP------ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 LLPAHNM--WTSTRFQEYLQRQGRGAVWGSVIYPSMK------KAIAHAMKVAQD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 RVKATGMDGTGSTNIDQFIQ---DAVKWVSFCYEGQERDATPEEMQRWRAFANEKKKENK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 DKEREATPA-----ELKEWRAFAQEQLKKDPEISPEHLKYAITDAIRAKMTGTGEATP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QALLNRI 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 AIQDKLRLERDGL--DAHSPANTDRFISEAIAWVNQCYDEKAPPPTEADMQHWRAFAADL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : | : | | | | | | 301 DISPEELKFAIQDAMRDEKMGTDAPASNRIEDHIRAAYGWLIYLNQAGPSQPSSEPT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 115; Gaps
                                                                                                                                                                                                                                                                                                                                                                Length 398;
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SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNGBER: US/08/596,300A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 1321-1-001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
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CORRESPONDENCE ADDRESS: ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 100.5; DB 2;
19.3%; Pred. No. 0.023;
tive 54; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AVEDLIEAEWEDLTQQYYSLVHGDAFISNSRNYFSQC--
FILE REFERENCE: 38-10(15849)B
CURRENT PEPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 E----TPLLICDTKFDIRQW----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 19.39
Matches 69; Conservative
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CITY: Hackensack
THATE: New Jersey
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                                                                                                                                                                                                                                                                                                         48 --LLARITSVNPQTDIDG-LRNIWIIKPAAKSRGRDI----VCMDRVEEILELAAADHPL 100
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                                                                                                                                                                                                                                                                                                                                                                           101 SRDNK--W------DWNPTIETPLLICDTKFDIRQWFLVT-----DWNPLTIW 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 SDGSLAEOFDKDSG-APLSATHLTWSYASFLSAAARRA-GIVPPSWGAASANSLPGSCS- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PANLTPASTTVTPPTQTGCAADHE 525
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                           40; Mismatches 126; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                           141 -------FYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKY---
                                                                                                                                                                                DB 1; Length 626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of Heterologous Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,300A
FILING DATA:
CLASSIFICATION: 435
                                                                                                                                                                                                                                           4 DTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQA
                                                                                                                                                                             6.0%; Score 94; DB 1
20.1%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1321-1-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08596300A Patent No. 5834191 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7: 411 Hackensack Avenue
Hackensack
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 14:
             SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                           72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 ASTVAGSYATATATŠĖ
                                                                                            protein
NO
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
TITLE OF INVENTION: Prov
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          Best Local Similarity
Matches 72; Conserva
                                                                                          MOLECULE TYPE:
                                                                                                                              FRAGMENT TYPE:
                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-596-300A-14
                                                                                                                                           US-08-596-300A-7
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STATE: NE
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                                                                                                                                                                             Query Match
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US-09-248-796A-20939

i Sequence 20939, Application US/09248796A

j Pattent No. 6747137

delance 20939, Application US/09248796A

j Pattent No. 6747137

delance 20939, Application US/09248796A

j Pattent No. 6747137

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC,

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/0/248,796A

CURRENT PILING DATE: 1998-02-12

PRIOR PILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208

SEQ ID NOS: 20939
                                                                                                                                                                                                                                                                                                                                                       17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             267 GYIISNFVNYRSGKDINSVLTSIHNFDPAA---GCDVNTFQPCSDR-----ALANHKV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: | :: :: :| 317 VVDSMRFWGVNSGRTAGKAAAVGRYAE-----DVYYNGNPWYLATLAAAEQLYDAVYVW 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 --LLNRITSVNPQTDIDG-LRNIWIIKPAAKSRGRDI----VCMDRVEBILELAAADHPL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----UVQKYIETPLLICDTKFDIRQWFLVT-----DWNPLTIW 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 KKQGSITVTSTSLAFFKDLVPSVSTGTYS--SSSSTYTAIINAVTTYADGFVDIVAQYTP 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 -----LKNDVGRSPLLPAHNWWTSTRFQEYLQRQGRGAV---WGSVIYPSMKKAIAH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 SDGSLAEQFDKDSG-APLSATHLTWSYASFLSAAARRA-GIVPPSWGAASANSLPGSCS- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 FTGLTKFQVTLILRHLYGVSNESLLDCFQYDFGEKDYFINDLLELIEVADELLLFQLKSV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 DAFODLLNSNTGDVV---IKASDGDVFAHAFVLKARSAFFETLLSERWDTEEKGNVQYVD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 -----SQCQALLNRITSVNPQTDID-----GLRNIWIIKPAAKSRGRDIVCMDRVEEI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------PANLTPASTTVTPPTQTGCAADHE 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 ------FYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKY-------
                                                                                                                                                                                                                                                                                          6.0%; Score 94; DB 1; Length 626;
20.1%; Pred. No. 0.24;
tive 40; Mismatches 126; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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20.8%; Pred. No. 0.42;
iive 45; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 DAVEDLIEAEWEDLIQOYYSLVHGD----AFISNSRNYF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 ASTVAGSYATATATSF-----
SEQUENCE CHARACTERISTICS:
LENGTH: 626 amino acids
TYPE: amino acidd
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 20.13
Best Local 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20939
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Matches 64; Conservative
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                                                                                                                                                                                                                                     US-08-596-300A-14
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193 TRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ-----DHVEPRKNS-FELYG
                                                                                                                                                                                                                                                                                                         4, 2006, 12:46:56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TI 139
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                                                                148 RFSTQRFSL-----DKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQ 202
                                                                                                                                                                                                                                                                                                         203 GRGAVWGSVIYPSMKKAIAHAMKVAQ--DHVEPRKNSFELYGADFVLGRDFRPWLIEINS 260
                                                                                                                                                                                                                                                                                                                                                       LELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDW----NPLTIWFYKESYL 147
                                                                                                                                                                                                          516 EIPNETMQLLEVFIDK-----LCN--VQNGTKNWIDQNPNILLEHIENIEEFNEYFMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-08-671-757A-7
Sequence 7, Application US/08671757A
Patent NO. 6476213
GENERAL INFORMATION:
APPLICANT: Suerbaum, Sebastian
TITLE OF INVENTION: Cloning and Characterization Production
of Aflagellate Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,757A
FILING DATE: 16-Aug_2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0073-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-671-757A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 24.19
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 SPTMHPS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       622 GESFPPT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-671-757A-7
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 RQCQALLMRITSVNPQTDIDGLRNIWIIKPAAKSRGRGESPDIVCMDRVEEILELAAADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDK
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    08igw4
08ipb2
08cfv5
08cfv5
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09plv5
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06eeh2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CAI42686.1; -; Genomic_DNA. GO; GO:0006483; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0006464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. Pfam; PF03133; TTL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q5JZ84_HUMAN PRELIMINARY; PRT; 747 AA.
Q5JZ84;
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
OTHUMPO0000028514 (Fragment).
ORFHUMDES=RP3-355C18.2-002;
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                      081PB2_DROME
Q8CT25_MOUSE
Q8CFV5_MOUSE
Q9CH88_MOUSE
Q9PIV5_HUMAN
Q9UPZ4_HUMAN
Q6EEF3_CERAE
Q5EFF3_CERAE
Q5EFF3_CERAE
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Q960F9_DROME
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Q4v8c1
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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08C0V2 MOUSE
09C0V1 MOUSE
1711.13 HUMAN
04KMS - HUMAN
09H876 - HUMAN
09H876 - HUMAN
09H871 MOUSE
058CT2 - BOVIN
0922T0 MOUSE
070156 - ANOGA
09VM91 DROME
07W92 DROME
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Q5F498_CHICK
Q9VKL9_DROME
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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28.1
26.5
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Score

Result Š 316

98

376 158 436

306.5 299 297.5

496

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CSTRAIN=C57BL/63; TISSUE=Testis;

NEDLINE=21085660; PubMed=11217881; DOI=10.1038/35055500;

A REDLINE=21085660; PubMed=11217881; DOI=10.1038/35055500;

A Arakawa T., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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Bronstein M.J., Bult C., Fletcher C., Fujita M., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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Savaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Marchionni K., Hasegawa Y., Kawaji H., Kohtsuki S.,

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Nordone P., Rodriguez C., Whittaker C., Wilming L.,

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Nordone P., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Wang K.H., Weitz C., Whittaker S.,
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                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930524K07 product:hypothetical Tubulin-tyrosine ligase
containing protein, full insert sequence.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

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Meth. Enzymol. 303:19-44(1999).
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                            518 AA
                                                                                                                                                                                                                                                                                                                                                     Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Testis;
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                      QBCOV2_MOUSE PRELIMINARY;
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Carricollide Secures 1. Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Pukuda S., Puruno M., Hanagaki T., Hara A., Hashizume W., Fukuda K., Puruno M., Hanagaki T., Haraoka T., Hirozane T., Harozane T., Katoh H., Kawai J., Kojima Y., Konno H., Kausuwa T., Katoh H., Kawai J., Kojima Y., Konno M., Roura M., Roya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nahi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibate K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (UJUL-2010) to the EMBL/Genbank/DDBJ databases.

Embel, AKO29745; BAC26595.1; -; mRNA.
Ensembl, ENSWUSGO00002388; Mus musculus.

RO; GO:0016874; F:ligase activity; IEA.

RO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933401B17 product:hypothetical Tubulin-tyrosine ligase
containing protein, full insert sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Muzinae; Mus.

NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 YGADFVLGRDFRPWLJEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDI
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SEQUENCE 518 AA, 59319 MW, 540C045659FACOD6 CRC64;
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80.5%; Pred. No. 1.3e-102;
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KRAINGESTORSEGO; PubMed=11217851; DOI=10.1038/3505500;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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SHEAIN-C578L/63; TISSUE-Testis;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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The FANTOM Consortium,
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Nature 420:563-573(2002).
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                   NUCLEOTIDE SEQUENCE
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NUCLEOTIDE SEOUENCE
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Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagaka A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO30151: BAC2611.1; -; MENA.

ENREML; AKO30151: BAC2611.1; -; MENA.

ENREML; MG1:1922902; 1700019901Rik.

GO; GO:0016849; F:1igase activity; IEA.

GO; GO:000644; F:lublin-tyrosine ligase activity; IEA.

GO; GO:000644; P:protein modification; IEA.

InterPro; IPR00434; Tub_Tyr_ligase.

EnterPro; IPR00434; Tub_Tyr_ligase.
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"Functional prediction of the coding sequences of 50 new genes deduced by analysis of cDNA clones from human fetal liver."; 
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDI 293
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
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TISSUE=Fetal liver;
Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ;
                                                                                                                                                                                                                                                                                                                                                                                   Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The German cDNA consortium;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       89398 MW; 9E98793C3351C3DE CRC64;
                                                                                                                                                                                                                                                                                         PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
Hypothetical protein; Ligase.
SEQUENCE 781 AA; 89398 MW; 9E98793C335LC3DE CR
                                                                                                                                                                                                                                                                                                                                                                                83.5%; Score 1303; DB 2;
80.5%; Pred. No. 2.2e-102;
ive 29; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-BUDlin tyrosine ligase-like protein 3 (HOTTL)
Name=TTLL3; ORFNames=PRO0207;
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Best Local Similarity
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             Matches
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EMBL; Bx648175; CAH10554.1; -; mRNA.
GO; GO:00064635; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IRR004344; Tub_tyr_lygase.
Pfam; PF03133; TIL; 1.
Hypothetical protein.
SEQUENCE 352 AA; 40257 MW; 49FD8E9CAEICB20D CRC64;
the Buropean Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVOKYIETPLLICDT
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                                                                                                                                                                                                                                                                              2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
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/FTId=VAR 020207.
I -> F (in Ref. 2).
: 49FDBEB118C7C20D CRC64;
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Last annotation update)
                                                                                                                                                                                                                               58.2%; Score 908; DB 1; 56.7%; Pred. No. 4.8e-69;
                                                                                                                                                                                                                                           ; Pred. No. 4.8e
48; Mismatches
                                                                          PIR; T12515; T12515.
Ensembl; ENSG00000156983; Homo sapiens.
                                                   EMBL; AL096725; CAB46375.1; -; mRNA.
EMBL; AF078842; AAF23353.1; -; mRNA.
                                                                                                   HGNC; HGNC:24483; TTLL3.
InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
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                                                                                                                                                                                                       40356 MW;
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QGAWA3;
                                                                                                                                                                                                                                                        Conservative
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290
                                                                                                                                      Ligase, Polymorphism.
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Matches 165; Conserv
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Length 352;

Score 908; DB 2;

58.2%;

Query Match

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TISSUE=PCR rescued clones;

X Strausberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

K Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A pitchul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A pitchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A., Gibbs R.A.,

Villaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Richards S., C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                     2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
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EMBL; BC098361; AAH98361.1; -; mRNA.
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Last sequence update)
Last annotation update)
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4.8e-69;
hes 78;
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56.7%; Pred. No. 4.8e
ive 48; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=PCR rescued clones;
NIH MGC Project;
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NIH MGC Project;
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Q4KMS8;
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NUCLEOTIDE SEQUENCE
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REPURE TISSUBE-PCR rescued clones;

RISTURE 2218825'; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Aluschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Aluschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Aluschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Aluschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wodin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abraamson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Richards S., Worley K.C., Soecegren B.J., Lu X., Glibbs R.A.,

R Allekseley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R "Generation and initial analysis of more than 15,000 full-length human and malman and
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                     DIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDM
                                                                                                                                                                                                                62 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                                                                                                                                                                                       KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                 2 DIDTSADAVEDLIEAEWEDLIQQYYSLVHGDAFISNSRNYFSQCQALLNRIISVNPQTDI
                                                                                                                                                                                                                                                                                                                                                           PLLPAHNWWTSTRFQEYLQRGGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 GADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRRLD 292
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                           Length 352;
                                                                                                           78; Indels
                      11 protein.
352 AA; 40381 MW; 49EF0C1118C7DD12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein DKFZp586B0320.
Name=DKFZp586B0320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                        58.2%; Score 908; DB 2; 56.7%; Pred. No. 4.8e-69; ive 48; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 AA
EMBL; BC099735; AAH99735.1; -; mRNA.
                                                                                                         Matches 165; Conservative
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Q8NDN8;
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                                                                                          Similarity
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                  Hypothetical
SEQUENCE 35
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                                                                        Query Match
                                                                                          Best Local
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QBNDN8_HU
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 PLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 GADFVFGEDFQPWLIEINASPTMAPSTAVTARLCAGVQADTLRVVIDRRLD 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78; Indels
                                                                                     Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AA; 49433 MW; 9E79E6CA08651CA1 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ13898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.2%; Score 908; DB 2; 56.7%; Pred. No. 6.2e-69; ive 48; Mismatches 78
                                                                                                                                EMBL, AL833939; CAD38794.1; -; mRNA.
EMBL, BCO89289; AH98298.1; -; mRNA.
GO; GO:0004835; F:tubulin-tyrosine ligase ac
GO; GO:0006464; P:protein modification; IEA.
InterPro; IRF004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 56.7%;
Matches 165; Conservative
rescued clones;
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TISSUE=PCR rescu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCHRH 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matenura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komateu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura Y., Okama V., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT--2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A630653H17 product:HOTTL PROTEIN homolog.
Name=4833441J24Rik;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Indels
                                                                                                                                                                                                                                                                GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
                                                                                                                                                                                                                                                                                                                                                                                         84683 MW; DF661753E4AFF0DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%; Score 908; DB 2; 56.7%; Pred. No. 1.2e-68,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches
                                                                                                                                                                                                            Nat. Genet. 36:40-45(2004).
EMBL; AK023960; BAB14741.1; -; mRNA.
Ensembl; ENSG0000156983; Homo sapiens.
                                                                                                                                                                                                                                                                                                                   nterPro; IPR004344; Tub_tyr_lygase.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.7%
Marches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                      Pfam; PF03133; TTL; 1.
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                         744 AA;
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                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Fukuda S.,
Arakawa T., Hara A., Fukumishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukumishi Y., Konno H., Adachi J., Yamanaka I.,
Andrawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Andra K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,
Andra M., Stabli F., Suzuki R., Tomita M., Wagner L., Washlo T.,
Schriml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washlo T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Bronstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
Aronstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Asasaki H., Toyo-oka K., Schoenbach C., Soya T., Shibata Y., Storch K.-F.,
Whynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaharana M., Waitz C., Whittaker C., Wilming L.,
Annaha, M., Marchioni K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha, M., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha, M., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha, M., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha, M., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha, M., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha M., Marchiola K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Annaha, Marchiola K., Kawaji H., Kawaji H., Kawaji H., Kohtsuki S.,
Annaha, M., Marchiola M., Handa M., Kawaji H., Kawaji H., Kawaji H.,
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Adachi J., Aizawa K., Akimura,
A Adachi J., Aizawa K., Akimura,
A Rukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Samo H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Toya T., Yayanishi A., Muramatsu M., Hayashizaki Y.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AKO80121; BAC37878.1; -; mRNA.
BENBENDI, SENWUSGO000003276; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE=Thymus; MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUB=Thymus; BDI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; DDI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiiwagi K., Fujiwake S., Inoue K., Togawa W., Tanaka T., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI; MGI:2141418; 4833441024Rik.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
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Gaps

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Indels

85;

44; Mismatches

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159; Conservative
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
M. Kellis M., Volff JW., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
The early vertebrate proto-karyotype.";
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                                                                                                                                                                                                                                    180
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                                                                                                                                                                                         |:|| |||:| |||:| ||| ||| 363 HPMLPPDNMWSSQRFQAHLQEVDAPKAWSSVIVPGMKAAVIHALQTSQDNVQCRKASFEL
                                                                                                                                           183 KÖIDKDPNSPLYLSPDDWSQFLQRYYQIVHEGAELRYLEVQVQRCEDILQQLQNVVPQLD
                                                                                                                                                                        61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                                1 EDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD
                                                                                                                                                                                                                                TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                           SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                 YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCD 292
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                          Length 704;
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                     76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 11 SCAF14979, whole genome shotgun sequence.
InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
SEQUENCE 704 AA; 79080 MW; 3FAD889C1DB5CF7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
; CAAE01014979; CAG06724.1; -; Genomic_DNA.
ENCE 534 AA; 60130 MW; 62B5BBBB696B662B CRC64;
                                                         Score 893; DB 2;
Pred. No. 2.1e-67;
54; Mismatches 76
                                                          57.2%;
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54.6%;
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                                                                                     Matches 162; Conservative
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Q4RY08;
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Score 855.5; DB 2; Length 534; Pred. No. 2.4e-64;

Best Local Similarity

Query Match

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322 KFDLRQWFLVTDWNPLTVWFYRECYLRFSTQPFSTKILDSSIHLCNNSIQKHFEPARNRH 381
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                                                             2 DIDTSADAVEDLIEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                           122 KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
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Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L.,
Harton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
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10-MAY-2005 (TYEMBLrel. 30, Last sequence update)
10-MAY-2005 (TYEMBLrel. 30, Last annotation update)
10-MAY-2005 (TYEMBLREL.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292
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SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 DIDIEEDT--KVWDHDWDVFLTHHYLLTHEDNRIQLLKEERBADAIEHYLAEAKSVLEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 TSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YLKNDVGRSPLLPAHNWWTSTRFQEYLQRGGRGAVWGSVIYPSMKKAIAHAMKVAQDHVE
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                                                                                                           YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCD 292
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-! -CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AAABO1008980; EAA13905.2; -; Genomic_DNA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006461; P:protein modification; IEA.
InterPro; IPR004341; Tub_tyr_lygase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Anopheles gambiae re-annotation.";
                                                                                                                                                                                                                                                                                                                                             ENSANGP0000022337 (Fragment)
                                                                                                                                                                                                                                                                                                                                                               ORFNames=ENSANGG0000019848;
                                                                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae str. PEST
                                                                                                                                                                                                                                    ANOGA PRELIMINARY;
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Best Local Similarity
Matches 135; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQRHLEASCHR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD 120
                                RSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFE
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
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                                                                                                             240 LYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC006830, AAH06830.1, -; mRNA.
Ensembl; ENSMUSG0000030276; Mus musculus.
MGI; MG1.2141418, 48334412481h.
GO; GO:00048435; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IPR004344; Tub_tyr_ligase.
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                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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61.0%; Pred. No. 2.1e-60;
iive 41; Mismatches 47;
                                                                                                                                                                                                                                             266 AA
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                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                    Q922TO MOUSE PRELIMINARY;
Q922TO;
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NUCLEOTIDE SEQUENCE.
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Gaps

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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002)

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RAY MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addams M.D., Celnikers S.E., Holt R.A., Evans C.A. Gocardos J. Celnikers S.E., Holt R.A., Evans C.A. Gocardos J. N., Radams M.D., Celnikers S.E., Richards S., Ashburner M., Henderson S.N., Burton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., R.A. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Clampe M., Pfeiffer B.D., Randon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D., R.A. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Miklos G.L.G., R.A. Ballew R.M., Basu A., Baxendale J., Rolfaraco C.R., Miklos G.L.G., R.A. Bellew R.M., Bans D. W., Berker B.G., Helf G., Nelson C.R., Miklos G.L.G., R.A. Bellew R.M., Bans P.V., Bernos D.A., Butler H., Cadieu E., Center A., Chandra I., R. Berts S. C., Busam D.A., Bullke C., Davenpott L.B., Davies P., Davies P., Doyon E.C., Dunn P., R.A. Borkova D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dordon K.J., Evangelista C.C., Ferraz C., Ferriera S., Pulkov B.C., Dunn P., R.A. Bouton E., Gorler M., Gabrielian A.E., Garraz C., Ferriera S., Pulkov B.C., Dunn P., R. Houston K.J., Evangelista C.C., Ferraz C., Ferriera S., Pulkov B.C., John P., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., A., Houston G.H., Ke Z., Kalp D., Lai Z., Liang Y., Lin X., Alalah M., Kalush F., Kalven G.H., Ke Z., Kannison J.A., Ketchum K.A., Alakon P., Murphy L., Murphy R., Murphy L., Murphy L., Murphy R., Balazolo M., Pittman G.S., Pan S., Pollard J., Warisen P.C., Siden-Klamos I., Simpson M., Skupeki M.P., Shu B., Spier E., Spradling A.C., Stapleton M., Skupeki M.P., Shu B., Shu B.C., Siden-Klamos I., Simpson M., Skupeki M., Wang Z.-Y., Wassarman D.A., Wolley K.C., Wu D., Yang S., Pan M., Wolgen P.C., Zhon W., Wang S., Zhu W., Wooder P., Zhong P.N., Zho
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MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nolson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstcok G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgum: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;

"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective."
                                                                                                              Name=CG1133; ORFNames=CG11323;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                      Last sequence update)
Last annotation update)
  992 AA.
                                               Created)
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                                                               01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
Q9VM91 DROME PRELIMINARY;
Q9VM91;
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461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 VHWPQYSLDGYQNMWIVKPANKCRGRGIILMDNLKKI--LGVVNLSIASKSRYVVQKYIE
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MEDLINE=22426069; PubMed=12537572;
MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                           Berkeley Drosophila Genome Project,
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
                                                                                                                                                                                         "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                                                                                Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. EMBL, AE003614; AAF53432.1; -; Genomic DNA. Ensembl; CG11323; Drosophila melanogaster. Flysase; FBGN031854; CG11323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0006464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase.
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                                                                                                                                                                                                         systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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Q7PMD3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 128; Conservative
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                                                                                                                                                                        Lewis S.E.;
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201 EDIDHEEFCEPLLTPENRHEMEQ----LLAGEAQFGSIPGYEVLSLVAQVKKLVHEAAKV 256
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                                                                                                                                                   P NUCLEALSTEENT.

G TRAIN-PEST.

G The Anopheles gambiae Sequence Committee;

L Submitted (APR-2004) to the BMBL/GenBank/DDBJ databases.

L CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

C EMBL, AAABO1008980; EAA13971.3; -; Genomic DNA.

DR GO; GO:0004815; F:tubulin-tyrosine ligase activity; IEA.

DR GO; GO:0004815; F:tubulin-tyrosine ligase activity; IEA.

DR GO; GO:0004815; F:tubulin-tyrosine ligase activity; IEA.

DR GO; GO:0004815; T:tubulin-tyrosine ligase

NINCEPTO; IPRO1761; ATP_GRASP.

DR HCEPTO; IPRO1313; TTL; 1.

DR PROSITE; PS50975; ATP_GRASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

34.6%; Score 539.5; DB 2; Length 501;
Best Local Similarity 41.1%; Pred. No. 2.3e-37;
Matches 123; Conservative 50; Mismatches 111; Indels 15
                                                                     The Anopheles gambiae Sequence Committee, "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    501 501
501 AA; 58862 MW; 806539A2FD8E76DF CRC64;
                                                                                                                                            NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=180454;
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4, 2006, 12:45:57

Search completed: April Job time: 45.3857 secs

calmodulin-binding

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April 4, 2006, 12:45:31; Search time 10.8922 Seconds (without alignments) 2588.231 Million cell updates/sec
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1 EDIDTSADAVEDLTEAEWED......LCAQVQEDTIKVAVDRSCDI 293
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                    OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	hypothetical prote	sine	protein ZK1128.6	hypothetical prote	hypothetical prote	protein C55A6.2 [i	hypothetical prote	tubulin-tyrosine l	hypothetical prote	_	probable US snRNP-	hypothetical prote	DNA strand transfe	glucan 1,4-alpha-g	glucan 1,4-alpha-g	hypothetical prote	gp330 protein prec	hypothetical prote	cyclic beta 1-2 gl		hypothetical prote		hypothetical prote	flagellar biosynth	integrin alpha-8 c	flagellar biosynth	hypothetical prote	fatty-acid synthas	probable mRNA guan
SUMMARIES	ID	T12515	A45443	E88575	T27699	T20262	C89217	T20343	T37571	A96805	S48261	T39188	T21403	S13743	T49625	S36364	T29116	T42737	T19049	H96974	E84317	T22615	T44806	F82885	E71937	S16516	A64650	T16367	S01787	T30703
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de	Query Match	58.2	16.4	15.6	15.6	13.4	13.4	10.6	10.3	10.0	9.3	6.1	6.1	6.1	9	0.9	6.0	5.9	5.8	5.7	9.6	5.6	5.6	2.6	9.6	9.6	5.5	5.5	5.5	5.5
	Score	908	255.5	244	244	209.5	209.5	166	160.5	155.5	144.5	95.5	95	94.5	94	94	93	91.5	90.5	83	88	87.5	87.5	87.5	87	87	86.5	86.5	86.5	98
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submitted to the EMBL Data Library, January 1995
A; Accession: T27699
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-680 < WILL>
A; Cross-references: UNIPROT: Q09647; UNIPARC: UPI000017A076; EMBL: Z47357; PIDN: CAA87425.2
A; Experimental source: clone ZK1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1198 «WIL»
A;Cross-references: UNIPROT:017720; UNIPARC:UP1000017A066; EMBL:281051; PIDN:CAB02862.2
A;Experimental source: clone C55A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CESP:C55A6.2
A;Map position: 5
A;Introns: 32/3; 68/1; 107/3; 201/3; 273/1; 364/3; 407/3; 460/3; 476/2; 534/2; 677/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGVANKPVPKWTLHHLW--EHFDEMGVDREKIQRE-----IEEVIIKAFISTEKPI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDH----VEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:| : | : | : | : | : | : 372 RAKFDLRLYAYVPIPEPLRVYIYDQGLVRFASVPYSHSVSTISNKYMHLTNYSINKLAEA 431
441 REHMSRFLEQEFICYELFGIDIILDEDYKPWLLEVNISPSLHSGTPLDVSVKAPLAKDVL 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK1128.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27699
R;Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Introns: 114/1; 208/3; 242/3; 334/3; 362/2; 405/2; 424/2; 550/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 15.6%; Score 244; DB 2; L. 1. Similarity 27.6%; Pred. No. 2.9e-13; 67; Conservative 48; Mismatches 90;
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Best Local Similarity
Matches 67; Conserva
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NLA 543
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A;Gene: CESP:ZK1128.6
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E88575
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID: 99069613; PMID: 9851916
A;Note: see websites genome. wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Molecule type: DNA
A;Mesidues: 1-640 <STO>
A;Cross-references: UNIPROT: Q09647; UNIPARC: UPI000017A077: CR.chr. 771. DITERLANDERCE
  A;Reference number: A45443; MUID:93147125; PMID:8093886
A;Accession: A45443
A;Btatus: preliminary
A;Retus: preliminary
A;Residus: 1-379 < RES>
A;Residus: 1-379 < RES>
A;Cross-references: UNIPROT:P38160; UNIPARC:UPI00001377A9; GB:X68453; GB:S54050; NID:921
A;Resimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:123858, NCBIP:123859)
C;Keywords: ligase
                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                151 TORFSLDKL-DSAIHLCHNAVOKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 SEPYHTDNFQDKTCHLTNHCIQKEYSKNYGK---YEEGNEMFFEEFNQYLT----SALN 276
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                                                                                                                                                                                                                                                                                                    36 SNSRNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAA
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                                                                                                                                                                                                                     Query Match
16.4%; Score 255.5; DB 2;
Best Local Similarity 28.4%; Pred. No. 1.3e-14;
Matches 74; Conservative 46; Mismatches 98;
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; Pred. No. 2.7e-13;
48; Mismatches 90;
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ilarity 27.6%;
Conservative 48
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Best Local Similarity
Matches 67; Conserv
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A,Map position: 3
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A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-662 < WILL.
A;Essidues: 1-662 < WILL.
A;Essidues: 1-662 < WILL.
A;Experimental source: clone D2013
A;Experimental source: clone D2013
A;Experimental source: clone D2013
A;Experimental source: Z19510
A;Reference number: Z19510
A;Accession: T2085
A;
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A;Refeace number: 221726
A;Refatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule: 17373
A;Residues: 1-403 - 4BAD>
A;Residues: 1-403 - 4BAD>
A;Residues: 1-403 - 4BAD>
A;Residues: 1-403 - 4BAD>
A;Cross-references: UNIPROT:Q10438; UNIPARC:UP1000013A94B; EMBL:Z70721; PIDN:CAA94694.
A;Experimental source: strain 972h-; cosmid c12B10
A;Experimental source: strain 972h-; cosmid c12B10
A;Experimental source: strain 972h-; hosmid c12B10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 NKVKFDLRYIVFLNGIAPVTAYVYNRFWIRFAINEFSLSNFEDVETHF---TVFNYL--D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 SADAVEDLTEAEWEDLTQQYYSL-VHGDAFISNSRNYFSQCQALLNRITSVNPQTDIDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 CDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKL-DSAIHLCNNAVQKYLKND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 YSLVHGDAFISNS-----RNYFSQCQALLNRITSVNPQTDIDGLRNI-----WIIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 662;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.6%; Score 166; DB 2; Lo
Best Local Similarity 24.3%; Pred. No. 2e-06;
Matches 72; Conservative 45; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%; Score 160.5; DB 2; 20.5%; Pred. No. 3e-06; live 61; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: CESP:D2013.9
A,Map position: 2
A;Introns: 78/2; 114/3; 330/3; 471/1; 521/2; 587/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Conservative
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Matches 63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein C55A6.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89217
R;anconymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Teference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A;Residues: 1-1203 <STO>
A;Cross-references: UNIPROT:O17720; UNIPARC:UPI000017A067; GB:Chr_V; PIDN:CAB02862.1;
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #text_change 09-Jul-2004"***
C;Accession: T20343; T22085
R;Mortimore, B.
R;Mortimore, B.
R;Mortimore, B.
R;Mortimore, B.
A;Reference number: Z19259
A;Accession: T20343
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                                                                                                                                                                                                                                           825 SSEDL--GHKWTLGALLRYVENEGKDA---KLLMLRIEDLIVKSLLSIQNSVATASRTNL 879
                                                                                                                                                                                                                                                                                                                                                          128 WFLVTDWNPLTIWFYKESYLRFSTQRF--SLDKLDS--AIHLCNNAVQK----YLKNDVG 179
                                                                                                                                                                                                                                                                                                                                                                                                                : || : || ::|| ::|| || ::|| || 3.4 || 3.4 || 3.4 || 3.5 || 3.4 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 WIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDTKFDIRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 RSPLLPAHNMWTSTRFQEYLQRGGRGAVWGSVIYPSMKKAIAHAMKVAQDHV--EPRKN-
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                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVA 286
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                          Length 1198;
                                                                                                          Indels
                      5;
                 13.4%; Score 209.5; DB 2
25.5%; Pred. No. 6.7e-10;
ive 57; Mismatches 87
                                                                                                          Conservative
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Matches 60: Conserv
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Matches 60; Conserv
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C,Genetics:
A,Gene: C55A6.2
A,Map position: 5
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A.Molecule type: DNA
A.Residues: 1-753 «MAN»
A.Cross-references: UNIPROT:P38254; UNIPARC:UPI000013A3DD; EMBL:X78993; NID:g476045; PI:
R.Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A.Reference number: S45927
A.Accession: S45962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 167-351, TPE', 356-449, 'A', 451-562, 'R', 564-753 <DEK>
A;Cross-references: UNIPARC:UP10000168D37; EMBL:X69881; NID:g4086; PIDN:CAA49508.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9UT24; UNIPARC:UPI00006BCA7; EMBL:AL121764; PIDN:CAB57421
A;Experimental source: strain 972h-; cosmid c9
                                                                                                                                                                                                                                                                                                                                                                     A;Cross_references: UNIPARC:UP1000013A3DD; EMBL:Z35963; NID:g536366; PIDN:CAA85047.1; A;Dekker, P.J.T.; Hoekert, W.; van Oosterum, K.; Grivell, L.A. submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable US snRNP-specific 200kd protein - fission yeast (Schizosaccharomyces pombe)
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                                                                         II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQ--EYLQRQGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          594 LDPYAYSVTDLKDLECHLTNTCLQS-KKKDKDSSVL------EFDSIEEIPNERKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
C;Accession: S48261; S45962; S41800; S44676
R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome A;Reference number: S48255; MUID:95208357; PMID:7900426
A;Accession: S48261
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 144.5; DB 2;
; Pred. No. 0.00018;
44; Mismatches 105;
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QTGKDLKNLIDELFDDTVKYCV 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3%;
21.8%;
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Best Local Similarity 21.84
Matches 57; Conservative
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A;Accession: S41800
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A; Residues: 1-2176 < WED>
                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-753 <FE2>
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A;Gene: SPDB:SPAC9.03c
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunger, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUD:21016719; PMID:11130712
A;Accession: A96805
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:Q9CAQ1; UNIPARC:UPI00000A09A3; GB:AE005173; NID:g6382502; P1
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                                                                                                                                                                                                                                                                                          DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLLPAHNMWISTRFQEYLOROG-----RGAVWGSV----IYPSMK---KAIAHAMK 225
                                                                                VQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAI---H 164
                                                                                                                                                                        165 LCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAM 224
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C;Date: 01-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T5M16.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
           SHODRAQGIRLESTIBELQAIFDSFDDEESESEEAGLEEKGDITVAFNNKIVISQIRNFL
                                                                                                             225 KVAQD----HVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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N;Alternate names: hypothetical protein YBR0821
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55; Conserv
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C;Genetics:
A;Gene: T5M16.14
A;Map position: 1
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Best Local
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submitted to the EMBL Data Library, November 1996
A; Reference number: 219418
A; Accession: T21403
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1217 <WILD>A; Cross-references: UNIPROT: Q9XV62; UNIPARC: UPI0000060FE4; EMBL: Z81513; PIDN: CAB04180.1; C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 5
A;Introns: 29/1; 568/2; 608/3; 746/1; 871/3; 910/1; 985/1; 1018/3; 1124/1; 1170/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F36D3.5
                                                                                                                                                  51 RITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQK 110
                                                                                                                                                                                                                                                                   :| |: | |: :| | :: | 340 -LENELM---SIFDYEHFYLVQLLTKNRWTIVSCTMLKRAATDEERLGVEEQIRAAGRSW 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SRLMSNKAVKLPEGSFRRTGKGYEEIHVPAPNKA 492
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---RSSLGQS 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRDNKWVVQKYIETPLLICD----TKFD----IRQWFLVTDWNPLTIWFYKESYLRFS 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F26D2.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21403
                                                                                            111 YIETPLLICDTKFDIRQWFLV----TDWNPLTIWFYK-------ESYLRFSTQRF
                                                               2 DIDTSADAVEDLTE---AEWEDLT------QQYYSLVHGDAFISNSRNYFSQCQALLN
                                                                                                                                                                           292 BIPTVHPR-EIDA---FWLQREIAKYFADAVVCQEKTNQAFEALSADYDLGE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.1%; Score 95; DB 2; Length 1217; Best Local Similarity 20.6%; Pred. No. 7.5; Matches 58; Conservative 49; Mismatches 106; Indels
  Pred. No. 15;
5; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 IDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 TFREPLSS------WNESLLKIL-----SAFOTAKPLWNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 VLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 VIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDF 251
                                                                                                                                                                                                                                                                                                                           155 SLDKL-----DSAIHLCNNAVQKYLKNDVGRSPL-
Similarity 19.1%; Pre 65; Conservative 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 NYVFTEG-----
Best Local Similarity
Matches 65; Conserva
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DNA strand transferase 2 - yeast (Saccharomyces cerevisiae)

NyAlternate names: DST2 protein; KEM1 protein; protein G1645; protein YGL173c; RAR5 pr
C;Species: Saccharomyces cerevisiae
C;Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C;Accession: S13743; S16701; S16885; S42156; S52457; A39790; S59238; S64190
C;Accession: S13743; S16701; Fink, G.R.
Genetics 126, 799-812, 1990
A;Title: kem mutations affect nuclear fusion in Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S13743
A;Molecule type: DNA
A;Cross-references: UNIPROT: P22147; UNIPARC: UPI000012DD97; EMBL: X54717; NID: g3846; PID
R;Tishkoff, D.X.; Johnson, A.W.; Kolodner, R.D.
Mol. Cell. Biol. 11, 2593-2608, 1591
A;Title: Molecular and genetic analysis of the gene encoding the Saccharomyces cerevis
A;Reference number: S16701; MUID: 91203880; PMID: 1840632
A;Accession: S16701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1528 «MOL»
A; Cross-references: UNIPARC:UPI000012DD97; GB:M58367; NID:g172579; PIDN:AAA35036.1; PI
R; Kipling, D.; Tambini, C.; Kearsey, S.E.
Nucleic Acids Res. 19, 1385-1391, 1991
A; Title: Rar mutations which increase artificial chromosome stability in Saccharomyces
A; Reference number: $16885; MUID:91227124; PMID:2027746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: S16868
A,Accession: S16868
A,Accession: S16868
A,Accession: S16868
A,Status: nucleic acid sequence not shown; translation not shown
A,Robiccule type: DNA
A,Robiccule the mucleoids sequence was submitted to the EMBL Data Library, August 1991
A,Note: the nucleoids sequence was submitted to the EMBL Data Library, August 1991
A,Accession: Structure of the XRNI exoribonuclease gene of Saccharomyces cerevisiae.
A,Description: Structure of the XRNI exoribonuclease gene of Saccharomyces cerevisiae.
A,Rocession: S42166
A,Accession: S42166
A,Accession: S4216
A,Accession: S4216
A,Accession: S4216
A,Accession: S4216
A,Accession: S2447
A,Accession: S2457
A,Accession: S2457
A,Accession: S2457
A,Accession: S2457
A,Accession: S2457
A,Accession: A3247
A,Accession: A3
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A.Residues: 1-1528 eBBW>
A.Residues: 1-1528 eBBW>
A.Residues: 1-1528 eBBW>
A.Cross-references: UNIPARC:UP1000012DD97; EMBL:X84705; NID:g677853; PIDN:CAA59180.1;
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
Submitted to the Protein Sequence Database, May 1996
A.Reference number: S64183
A.Reference number: S64183
A.Molecule type: DNA
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C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alph C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-19/Domain: signal sequence #status predicted <SIG> F;20-35/Domain: propeptide #status predicted <PRO> F;33-458/Domain: glucan 1,4-alpha-glucosidase homology <GAG> F;33-626/Product: glucan 1,4-alpha-glucosidase #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Koh-Laur, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Ainley, K.; Johansen, submitted to the Protein Sequence Database, January 1990
A;Description: Exported proteins of Neurospora crassa 1: - glucoamylase.
A;Reference number: S13711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-626 <STO.
A;Cross-references: UNIPARC:UPI000014A557; EMBL:X67291
A;Cross-references: UNIPARC:UPI000014A557; EMBL:X67291
R;Koh-Luar, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Ainley, K.; Johansen,
Enzyme Microb. Technol. 11, 692-695, 1989
A;Title: Exported proteins of Neurospora crassa: 1-glucoamylase.
A;Reference number: S13710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 KKQGSITVTSTSLAFFKDLVPSVSTGTXS--SSSSTYTAIINAVTTYADGFVDIVAQYTP 428
                                                                                                                                                                                                                                                                                                                                                                          Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Neurospora crassa N;Alternate names: glucoamylase; glycoamylase C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 31-Dec-1993 #text_change 02-Jun-2003 C;Accession: S36364; S13710; S13711; S25539
R;Stone, P.J.; Makoff, A.J.; Parish, J.H.; Radford, A.
Curr. Genet. 24, 205-211, 1993
A;Title: Cloning and sequence analysis of the glucoamylase gene of Neurospora (A;Reference number: S36364; MUID:94037144; PMID:8221928
                                             371 KKQGSITVTSTSLAFFKDLVPSVSTGTYS--SSSSTYTAIINÄVTTYADGFVDIVAQYTP 428
                                                                                                -----LKNDVGRSPLLPAHNWITSTRFQEYLQRQGRGAV---WGSVIYPSMKKAIAH 222
                                                                                                                                                429 SDGSLAEQFDKDSG-APLSATHLTWSYASFLSAAARRA-GIVPPSWGAASANSLPGSCS- 485
                                                                                                                                                                                                  AMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ALANHKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LLNRITSVNPQTDIDG-LRNIWIIKPAAKSRGRDI----VCMDRVEEILBLAAADHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                     ---PANLTPASTTVTPPTQTGCAADHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·FYKESYLRFSTORFSLDKLDSAIHLCNNAVQKY~
---FYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 36-60,'X',62,'X',64-65 <KOH>
A;Cross-references: UNIPARC:UP10000175ASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 36-60,'X',62,'X',64-65 <KOW>
A;Cross-references: UNIPARC:UP10000175A5C
                                                                                                                                                                                                                                                        486 ASTVAGSYATATATSF----
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20.1%;
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Best Local Similarity
Matches 72; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S13710
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N;Alternate names: protein B5022.70
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2003
C;Accession: T49625
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain; glucan 1,4-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: Z25022
A;Actession: 149625
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-626 <6207
A;Cross-references: UNIPARC:UPI000006A8CB; EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.70
A;Experimental source: BAC clone B5022; strain OR74A
                        Cross-references: UNIPARC:UPI000012DD97; EMBL:Z72695; NID:g1322777; PIDN:CAA96885.1;
                                                                                                                                                                                                                                                                                                                13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 LAAADHPLSRDNKWVVQKYIETPLLICDTKFDIR------QWFLVTDWN--PLTIW 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
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                                                                                                                                                                                                                                                                                                                                                                                                501 KTIYN---ERFERWKHEYYHDKLKFTTDSEEKVRDLAKDYVEGLOWVLYYYYRGCPSWSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 FYKESYL-RFSTQ-----RFSLDKLDSAIHLCNNAVQKYLKNDVGRS--PLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYPHHYAPRISDLAKGLDQDIEPDLSKPFTPFQQLMAVLPERSKNLIPPAFRPLMYDEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAHNMWISTRFQEYLQRGGRGAVWGSVIYPSM--KKAIAHAMKVAQDHVEPRKNSFELYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                  43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 ADFVLGRDFRPWLIBINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRS 290
                                                                                                                                                                                                                                                          Length 1528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: NCSP:BSO22.70
A,Map position: 6
A,Introns: 301.1
C,Superfamily: glucan 1,4-alpha-glucosidase with starch-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 626;
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                                                                                                                                                                                                                                                             Query Match 6.1%; Score 94.5; DB 2; Best Local Similarity 20.5%; Pred. No. 11; Matches 59; Conservative 54; Mismatches 132;
A;Residues: 1-1528 cBRU>
A;Cross-references: UNIPARC;UPI000012DD97; EMBL:Z7269;
A;Experimental source: strain S288C
C;Genetis:
A;Genetis:
A;Genetis:
A;Genetis:
A;Genetis:
A;Cross-references: SGD:S0003141; MIPS:YGL173C
A;Map position: 7L
C;Superfamily: Schizosaccharomyces pombe exonuclease:
C;Keywords: nucleus
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Best Local Similarity
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C; Genetics:
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174LKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAH 222	429 SDGSLAEQFDKDSG-APLSATHLTWSYASFLSAAARRA-GIVPPSWGAASANSLPGSSCS- 485	223 AMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQE 280	486 ASTVAGSYATATATSFPANLIPASTTVTPPTQTGGAADHE 525
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Search completed: April 4, 2006, 12:51:53 Job time : 12.8922 secs

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- protein search, using sw model OM protein

April 4, 2006, 12:42:35

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd

; Search time 93.4006 Seconds (without alignments) 1378.343 Million cell updates/sec US-10-635-977-2_COPY_73_365 1560 Title:

1 EDIDTSADAVEDLTEAEWED......LCAQVQEDTIKVAVDRSCDI score: Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters:

2443163 seqs, 439378781 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2003bs:* geneseqp2004s:* geneseqp2002s:* geneseqp2003as:* geneseqp2005s:* A_Geneseq_21:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	uc	Human BGS	Human tub			Human ORF	Human pol	Human HOT	Pumour-as	Human MDD	Human cyt	Human pro	Human pro		Human HOT	Drosophil	Human pro	Drosophil	Human pol			Human mol	Human nov	Drosophil	Drosophil
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SUMMARIES	ΙD	ADJ93366	ADJ93365	ADJ93358	ADJ93360	AAB43005	AAM39450	ADJ93457	ABM80420	ABU11512	AAU74334	AAB94796	ADM05524	AAB58909	ADJ93455	ABB65645	ABU92048	ABB65541	AAM41236	ADQ66614	ABG05971	ADH45424	ABU00150	ABB64074	ABB60840
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d	Query Match	100.0	100.0	100.0	79.9	58.2	58.2	58.2	58.2	58.2	58.2	58.2	58.0	57.5	52.4	40.8	39.3	33.0	30.8	28.1	24.0	21.5	21.2	20.8	19.1
	Score	1560	1560	1560	1247	908	908	908	908	908	908	908	905	897	817	636	613	515.5	480	439	374	336	330	324	297.5
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SULT 1 J93366 ADJ93366 standard; protein; 293 AA.	ADJ93366;	06-MAY-2004 (first entry)	Human BGS-42 protein-related TTL1 domain.	testis-specific tubulin tyrosine-ligase-like polypeptide; BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory, anabolic; hypertensive; osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic; anti-HIV; antibacterial; immunosuppressive; antiseborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; testicular cancer; pulmonary disorder; lung cancer; gastrointestinal disorder; colon cancer; promach cancer; neural disorder; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease, acromegaly; Alzheimer's disease; Parkinson's disease; immunological disorder; arthritis; asthma; AIDS; sepsis; acne; Sjogren's disease; scleroderma; human; TIL1 domain.
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ALIGNMENTS

Homo sapiens

WO2004005487-A2.

15-JAN-2004.

09-JUL-2003; 2003WO-US021605.

8 (BRIM) BRISTOL-MYERS SQUIBB

2002US-0394725P.

09-JUL-2002;

Wu S, Nelson TC; Feder JN,

WPI; 2004-099381/10.

e.g. New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular

Disclosure; SEQ ID NO 14; 343pp; English.

disorders.

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This invention relates to a novel testis-specific tubulin tyrosine-ligase compared the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory gestrointestinal-Gen, neuroprotective, endocrine-Gen, respiratory cantinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiathritic, antiasthmatic, antiharty acting as tyrosine ligase modulators. In addition, the disclosed sequences may be tyrosine ligase modulators. In addition, the disclosed sequences may be tyrosine ligase modulators. In addition, the disclosed sequences may be useful for disponsing a pathological condition, the disclosed sequences may be compared to a pathological condition, such as a disorder related to aberrant cubulin ligase activity, a disorder related to aberrant tubulin.

CC ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin.

CC arboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, pulmonary disorders, testicular disorders, testicular cancer, pulmonary disorders, concurs disorders, transcribity, aberrant cellular proliferation cof the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide can be used as a preventive agent for immunological conservationing infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptides. The present sequence is that of the TIL1 domain of the human BGS-42 protein of the invention.
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120 180 9 EDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD TKFDIROWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 1 EDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD 0; Gaps Length 293; Indels 2.8e-160; DB 8; ö Query Match 100.0%; Score 1560; Best Local Similarity 100.0%; Pred. No. 2.8 Matches 293; Conservative 0; Mismatches 121 ò g ò g 8

Sequence 293 AA;

240 SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 240 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 293 241 181 181 241 ద g ò ò 유

ADJ93365 standard; protein; 541 AA. 06-MAY-2004 (first entry) ADJ93365; ADJ93365

Human tubulin tyrosine ligase protein consensus sequence SeqID13.

testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase moddlator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;

gastrointestinal disorder; colon cancer; stomach cancer; neural disorder; brain cancer; liver cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; immunological disorder; arthritis; asthma; AlDS; New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular sepsis; acne; Sjogren's disease; scleroderma; human. (BRIM) BRISTOL-MYERS SQUIBB CO. 09-JUL-2002; 2002US-0394725P. 09-JUL-2003; 2003WO-US021605 Nelson TC; WPI; 2004-099381/10. N-PSDB; ADJ93364. Wu S, WO2004005487-A2. Homo sapiens. 15-JAN-2004 Synthetic. Feder JN, disorders.

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Example 4; SEQ ID NO 13; 343pp; English.

This invention relates to a novel testie-specific tubulin tyrosine-ligase
-like polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
cen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,
antiparkinsonian, antiarthritic, antiasthmatic, anti-Har, antibacterial,
antiparkinsonian, antiarthritic, antiasthmatic, antibacterial,
immunosuppressive, antiseborrineic or dermatological activity acting as
tyrosine ligase modulators. In addition, the disclosed sequences may be
useful for gene therapy. The BGS-42 polypeptide or polymuclectide can be
useful for diagnosing a pathological condition or a susceptibility to a
pathological condition, such as a disorder related to aberrant
tubulin ligase activity, aberrant cellular proliferation, reproductive
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, colon cancer, pulmonary disorders,
lung cancer, gastrointestinal disorders, colon cancer, promoch cancer,
neural disorders, brain cancer, liver cancer, pulmonary disorders,
cof the testis, lung, small intestine, brain or lymph tissue. The BGS-42
polypeptide, polymucleotide, or their modulators are also useful for
treating infertility, Cushings syndrome, emphysema, pneumonia, Addison's
disorders including arthritis, asthma, AIDS, sepsis, acne, signer, and
casses acroomegaly, Alaheimer's disease, or Parkinson's disease or sclenoderma. The antibodies may be used to purify, detect and
casses or sclenoderma. The antibodies may be used to purify, detect and
cancer the BGS-42 polypeptides. The present sequence is that of the
tubulin tyrosine ligase protein consensus sequence which was used in the tubulin tyrosine ligase protein coemplification of the invention.

Sequence 541 AA;

ö 132 09 1 EDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTD Gaps ö 100.0%; Score 1560; DB 8; Length 541; Indels Score rock,
Pred. No. 7e-160; 0; Mismatches 100.0%; 293; Conservative Similarity Query Match Best Local S Best_Loca Matches

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192 61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD

carboxypeptidase activity, a disorder related to aberrant tubuling amedical condition, tuch as a disorder related to aberrant tubuling a cutivity, a disorder related to aberrant tubuling tubulin ligase activity, a disorder related to aberrant tubuling carboxypeptidase activity, activity and carboxypeptidase activity, activity and cancer, pulmonary disorders, lung cancer, pulmonary disorders, lung cancer, particular cancer, pulmonary disorders, lung cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including archritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 protein of the invention.

pathological condition in a subject, and for preventing, treating

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Hestis-specific tubulin tyrosine-ligase-like polypeptide;

BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;

BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;

M neuroprotective; endocrine-Gen; antiafhratic; antiasthmatic;

M steopathic; nootropic; antiparkinsonian; antiathritic; antiasthmatic;

M anti-HIV; antibacterial; lumunosuppressive; antiastborrheic;

M ermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;

tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;

testicular disorder; testicular cancer; pulmonary disorder; lung cancer;

M prain cancer; liver cancer; proliferative condition; testis; lung;

M small intestine; brain; lymph tissue; infertility; Cushing's syndrome;

emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;

M sepsis; acne; Sjogren's disease; scleroderma; human.
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                                                           240
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                TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                         SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                              313 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 365
                                                                                                               YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 293
                                                                                                                                                                                                                                                                                                         Human BGS-42 protein sequence SeqID2.
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                                                                                                                                                                                                                   ADJ93358 standard; protein; 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelson TC;
                                                                                                                                                                                                                                                                             (first entry)
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N-PSDB; ADJ93357.
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BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; concert, neural disorder;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia, Addison's disease; acromegaly; Alzheimer's disease;
sextingon's disease; immunological disorder; arthritis; asthma; AIDS;
sepsis; acne; Sjogren's disease; sclerodexma; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 SPLLPAHNMYTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 SPLLPAHNMWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 1560; DB 8
100.0%; Pred. No. 7e-160;
ive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 293; Conservative
                                                                                                                                                                                                                                                                                    Sequence 541 AA;
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This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory -GGN, gastrointestinal-GGN, neuroprotective, endocrine-GGN, antiinflammacory, anabolic, hypertensive, osteopathic, nootropic, antiinflammacory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial, immunosuppressive, antiseborrheic or dermacological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppessant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianaemic; gene therapy; cancer; proliferative antihhyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; servere combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;

Human ORFX ORF2769 polypeptide sequence SEQ ID NO:5538.

(first entry)

08-FEB-2001

AAB43005;

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This invention relates to a novel testis-specific tubulin tyrosine-ligase

-like polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory

-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

antinflammatory, anabolic, hypertensive, osteopathic, nootropic,

antingarkinsonian, antiathritic, antiasthmatic, anti-HIV, antibacterial,

immunosuppressive, antiseborrheic or dematological activity acting as

tyrosine ligase modulators. In addition, the disclosed sequences may be

cytosine ligase modulators. In addition, the disclosed sequences may be

cytosine ligase modulators. as useful to a subject, and for preventing, treating or

cused for disgnosing a pathological condition or a susceptibility to a

pathological condition in a subject, and for preventing, treating or

cused for disgnosing a pathological condition, such as a disorder related to aberrant

cused for disgnosing a medical condition, such as a disorder related to aberrant

completing a medical condition, such as a disorder related to aberrant

composition ligase activity, aberrant cellular proliferation, reproductive

disorders, testicular disorders, testicular cancer, pulmonary disorders,

lung cancer, gastrointestinal disorders, colon cancer, stomach cancer,

carboxypeptides activity, aberrant cellular proliferation cof the testis, lung, small intestine, brain or lymph tissue. The BGS-42

polypeptide can be used as a preventive agent for immunological

cy testing infertility, Cushing's syndrome, emphysema, pneumonia, Addison's

disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42

cy disease or scleroderma. The antibodies may be used to purify, detect and

cy disease or scleroderma. The present sequence is that of the human

cy polypetide can be used as a preventive agent to their purention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 4; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                       09-JUL-2003; 2003WO-US021605.
                                                                                                                                                                                                                                   09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feder JN, Wu S, Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-099381/10.
15-JAN-2004.
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61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 120
                                                                                                                                                                                                                                                                                                                                       1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVKYIETPLLICD
                                                                                                                                                                                                                                                                                                                                                        TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                 181 SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                241 YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 293
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                                                                                                                                                                                                                                                                                                       79.9%; Score 1247; DB 8; Length 242; 100.0%; Pred. No. 2.2e-126;
                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                            Sequence 242 AA;
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                                                                                                                                                                                                                                                                                                        Query Match
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AAB43005 standard; protein; 352 AA.

RESULT 5

180

9

Gaps

240

120

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
cantipsoriatic; antiparkinsonian; nootropic; hepatotropic; vulnexary;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
cardiant; thrombolytic; antithermatic; antidiabetic; hypotensive;
cardiant; thrombolytic; antithermatic; antidiabetic; hypotensive;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
cardiant; thrombolytic; antithyroid; and antidiabeterial;
antifundal; antithermatic; antithyroid; and antidiabeterial;
cardianted is at reading pathological conditions associated with an operating or treating pathological conditions associated with an operation or preventing or treating pathological conditions associated with an operation of the nucleic acids can be used to express ORFX
conficens in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft va host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
corrage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AlDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 4720-4721; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 165; Conservative
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Best Local S
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frame X,

02-APR-1999; 99US-0127636P. 05-APR-1999; 99US-0127728P. 30-MAR-2000; 2000US-00540763.

Leach M;

Shimkets RA,

WPI; 2000-602362/57. N-PSDB; AAC77214.

(CURA-) CURAGEN CORP.

99US-0127607P

31-MAR-1999;

31-MAR-2000; 2000WO-US008621

thrombosis; contraceptive.

WO200058473-A2

05-OCT-2000.

Homo sapiens

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in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous injuries, peripheral nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, ancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leuksemias and sasays for receptor activity, arthritis and inflammation, leuksemias and C.N.S disorders. Note: The sequence data for this patent did not form
 immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein sequence SeqID2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ93457 standard; protein; 352 AA
                                                                                                                                                                               part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.7
Matches 165; Conservative
                                                                                                                                                                                                             Sequence 352 AA;
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              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; handrington's disease; handrington's disease; handrington's disease; hamostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                   Wang D;
, Zhao (
                          DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                             KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                        PLLPAHNMWTSTRFQEYLORGGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
          DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                  GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292
                                                                                                                                                                                                                                                                     242 GADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRRLD 292
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Zhang J,
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Yang Y,
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Xue AJ,
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                                                                                                                                                                                                                                                                                                                                                        AAM39450 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang Z, Wehrman T, Xu (Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 2595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552117.
20-UIN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US034263.
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Wang Z, Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Althélmer's disease;
parkinson's disease; immunological disorder; arthritis; asthma; AlDS;
sepsis; acne; Sjogren's disease; scleroderma; human; HOTFL3.
                                                                                                                     61
                                                                                                        2 DIDKOLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDM
                                                                                                                                                                                  KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                               2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                        PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                           62 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDT
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 352;
                                       78; Indels
58.2%; Score 908; DB 4; 56.7%; Pred. No. 2.6e-89;
                                     48; Mismatches
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ABM80420 standard; protein; 352 AA

ABM80420

(first entry)

18-NOV-2004

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ABM80420;

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This invention relates to a novel testis-specific tubulin tyrosine-ligase complete to the development of compounds with a cytostatic, respiratory to be useful for the development of compounds with a cytostatic, respiratory. Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, noctropic, antiinflammatory, anabolic, hypertensive, osteopathic, noctropic, antiinflammatory, anabolic, hypertensive, antiinflammatory, anabolic, hypertensive, antiinflammatory and antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be consetul for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a cused for diagnosing a medical condition, such as a disorder related to aberrant tubulin-carboxypeptidase activity, a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptidase activity, aberrant cellular proliferation, reproductive carboxypeptides activity, aberrant cellular proliferation, reproductive carboxypeptides prain cancer, liver cancer, scomach cancer, lung cancer, gastrointestinal disorders, colon cancer, scomach cancer, contained cancer, pulporated, polymecleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromagaly, Alzheimer's disease, or Parkinson's disease. The BGS cateroderms including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or acleroderman The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the human cancer are appeared to the invention. Note: The present concerned by the present in the specification but was obtained from
                                                                                                                                                                                                                                New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 7; 343pp; English
                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
                      09-JUL-2002; 2002US-0394725P.
                                                                                                                            Nelson TC;
                                                                                                                                                                              WPI; 2004-099381/10.
                                                                                                                               wu s,
                                                                                                                                                                                                                                                                                                                      disorders.
                                                                                                                               Feder JN,
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122 KFDIROWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVQKYLKNDVGRS 181 DIDKDLBAPLYLTPEGWSLFLORYYOVVHEGAELRHLDTQVORCEDILQOLOAVVPOIDM PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY 2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT Gaps GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292 ; 0 58.2%; Score 908; DB 8; Length 352; 56.7%; Pred. No. 2.6e-89; Indels 48; Mismatches Best Local Similarity 56.79 Matches 165; Conservative Sequence 352 AA; 62 62 182 242 Query Match ò 셤 ઠ 셤 8 유 à g

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acids and antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosing of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with concreased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cancer, cancers of the central cancer, pancreatic cancer, cervical cancer, cancers of the central cancer manners and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in the present sequence
                                                                                                                    Tumour-associated antigenic target (TAT) polypeptide PRO80956, SEQ:1058.
                                                                                                                                                            antigenic target; TAT; human; overexpression; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                  tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; SEQ ID NO 1058; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2002; 2002US-0414971P
                                                                                                                                                                                                                                                                                                gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TD, Zhang Z, Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-347921/32.
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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ö 62 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT 121 61 61 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI Gaps Length 352; 78; Indels 58.2%; Score 908; DB 8; 56.7%; Pred. No. 2.6e-89; iive 48; Mismatches 76 165; Conservative Similarity Sequence 352 AA; Query Match Best Local S Matches ò 셤 8

represents a TAT polypeptide of the invention

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RESULT

242 GADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRMLD 292

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                 121
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                                                                                                                                                                                                                                                                                                                   MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; call proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                     PLLPAHINMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
J. Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
JS. Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
JH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel disease detection and treatment me polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
                                                                                                                                                 GADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 459; 339pp + Sequence Listing; English.
                                                                                                                                                                                                                         Ŕ
                                                                                                                                                                                                                                                                                              Human MDDT polypeptide SEQ ID 459.
                                                                                                                                                                                                                     ABU11512 standard; protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
17-MAY-2001; 2001US-0299428P.
20-JUN-2001; 2001US-029976P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2002; 2002WO-US009944
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                                                                                                                                                                                                                                                                       (first entry)
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Peralta CH, David MH,
Flores V, Marwaha R,
                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis; hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-058431/05.
N-PSDB; ABX34502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200279449-A2.
                                                                                                                                                                                                                                                                      12-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dufour GE,
                                                                                                                                                                                                                                             ABU11512;
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osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and hepatotropic activity. The polymucleotides cand the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are conditions. These polypeptides or polymucleotides are conditionally useful for diagnosing, treating or preventing call proliferative disorders (e.g. cancers including adenocarcinoma, proliferative disorders (e.g. cancers including adenocarcinoma, cleakaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's cleakaemia, lymphoma, melanoma, myeloma or sarcoma), anoemia, Crohn's cleakaemia, lymphoma, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABU11450-ABU11845 represent the MDDT polymucleotides encoded cy ABU11450-ABU11845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder; cell proliferative disorder; inflammatory disorder; prion disease; vesicle trafficking disorder; gastrointestinal disorder; muscle disorder; neurological disorder; cell motility disorder; reproductive disorder; spinal cord disease; central nervous system disorder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 KFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          58.2%; Score 908; DB 6; Length 399; 56.7%; Pred. No. 3.1e-89; ive 48; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cytoskeleton-associated protein (CYSKP) #5.
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2000US-0209705P.
2000US-0210149P.
2000US-0213215P.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.7
Matches 165, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200185942-A2
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05-JUN-2000;
07-JUN-2000;
21-JUN-2000;
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「人」を発力をある

Charles Care

Human; primer; detection; diagnosis; antisense therapy; gene therapy

Homo sapiens EP1074617-A2 07-FEB-2001. 28-JUL-2000; 2000EP-00116126

Human protein sequence SEQ ID NO:15921

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The invention relates to human cytoskeleton-associated polypeptides

(CYSKP) and their associated polymucleotide sequences. The sequences are useful in the treatment of disorders associated with overexpression or underexpression of CYSKP in a patient. The disorders include cell

conditionally an expectation of CYSKP in a patient. The disorders include cell

conditionally conditionally concern as asthma, atherosciences, arteriosclerosis, crohn's disease, rheumatoid arthritis, diabetes mellitus

conteoporosis, crohren's disease, neurological disorders (such as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,

cond other motor neuron disorders), cell motility disorders, reproductive disorders (such as endometriosis and polycystic ovary syndrome), muscle disorders (such as myocarditis, migraine, hypertension, hypoglycaemia, myocardial infarction, epilepsy and muscular disorders (such as pown syndrome and cerebral palsy) and mental disorders (such as anxiety and schizophrenia).

conteoporosis and mental disorders (such as anxiety and schizophrenia).
                                                                                        Kearney L;
                                                                                                                                                                                                                                New cytoskeleton-associated proteins and polynucleotides, useful for diagnosing, preventing and treating cell proliferative, autoimmune, inflammatory, neurological, cell motility, reproductive and muscle
                                                                Hillman JL;
Batra S, 1
                                                                  Baughn MR,
Burford N,
                                                                  , Lu DAM, 1
Bandman O,
                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 130-131; 194pp; English.
                                                                  Au-Young J,
                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                WPI; 2002-062248/08
                                                                                        Lal P,
                                                                                                                                                                                           N-PSDB; AAS99894
                                                                  Tang YT,
                                                                                                                 Policky JL;
                                                                                             Azimzai
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EGDRNIWIVKPGAKSRGRACMDHLEEMLKLVNGNPVVWKDGKWVVQKYIERPLLIFGT 121
                                                                                                                                                                                              KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS 181
                                                                                                                                                                                                                 ріркріваргуітресизігідкуй уунедавінні ртоудкорі догоду бі
                                                                                                                               DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                                                                                                                                                                 PLL.PAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                               2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                                                      GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292
                                .;
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 Length 488;
                              78; Indels
58.2%; Score 908; DB 5; 56.7%; Pred. No. 4.2e-89;
                             48; Mismatches
                                  Conservative
               Best Local Similarity
Matches 165; Conserv
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   Query Match
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Sequence 488 AA;

AAB94796 standard; protein; 744

RESULT 11 AAB94796 (first entry)

26-JUN-2001

AAB94796;

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The present invention describes primer sets for synthesising 5602 full-

(a) an oligo-dr primer and an oligonaclectide complementary to the

complementary strand of a polynucleotide which comprises one of the 5602

complementary strand of a polynucleotide which comprises one of the 5602

complementary strand of a polynucleotide which comprises one of the 5602

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide of sequence complementary to a

complementary strand of a polynucleotide of sequence complementary to a

complementary strand of a polynucleotide of sequence of of the primers and path 13632 to AAH13632 represent conservation of the conservation of the exemplification of the exemplement of the exemplification of the exemplements of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; SEQ ID NO 15921; 2537pp + Sequence Listing; English.
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Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.2%; Score 908; DB 4; 56.7%; Pred. No. 7.8e-89; ive 48; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ogai T, Nishikawa T, Hayashi K, S.
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                              27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.79
Matches 165; Conservative
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122 KFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCHRH 181

242 GADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292

AAB58909 standard; protein; 362 AA.

RESULT 13

PLLPAHNWWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY

182 182

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453
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM0136 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                   PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
                                                                                   GADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRMLD
                                                                 GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD
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                                                                                                                                                                                                                                                                                                                            human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                           Human protein of the invention SEQ ID NO:4209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 4209; 305pp; English
                                                                                                                                                                                     ADM05524 standard; protein; 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2002; 2002EP-00008400.
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                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 56.7'
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J, Isono Y,
Yoshikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 326 AA;
                                                                                                                                                                                                                                                                                                                                                                                            EP1347046-A1.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                          20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T,
                                                                                                                                                                                                                         ADM05524;
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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AABS9111 - AABS9128. The DNA and protein sequences are graculated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and ABES9129 which are used in the invention are sequences AAF22032 - AAF22040 and ABES9129 which are used in the cancer and ovarian cancer associated DNA, protein, agonist cor antagonist sequences exhibit cyrcatatic; immunosuppressive; noctropic; or antagonist sequences exhibit cyrcatatic; immunosuppressive; noctropic; cor antipidiammatory; anticuler; vulnerary; anticorvulsant; anticiabetic; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly correst and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's classes, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as cerebral anoxia and epilepsy; and
                                                                                                        Breast and ovarian cancer associated antigen protein sequence SEQ ID 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and disgnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                       nootropic, neurpprotective, antiviral; antiallergic; hepatofropic; antidabetic; antiinflammatory, antiuloer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabbetes mellitus; Crohn's disease; multiple sclerosis; rheumacoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1056-1057; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270P.
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-611515/58.
N-PSDB; AAF21812.
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                               27-MAR-2001
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61

Gaps

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DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT 121

62 62

2 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 61

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122 KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS 181

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26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; plemonary disorder; neural disorder;
gastrointestinal disorder; colon cancer; promach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; arthritis; asthma; AlDS;
                                                                                                                                                                               132
                                                                                                                                                                                                                                              192
                                                                                                                                                                                                                                                                                                             252
                                                                                                                                                                                                                                                                                                                                           210 ORFOAHLOEMGAPNAWSTIIVPGMKDAVIHALQTSQDTVQCRKASFELYGADFVFGEDFQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular disorders.
                                                                                                                 72
                                                                                                               13 LTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKP
                                                                                                                                   73 AAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVT
                                                                                                                                                                                               DWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTS
                                                                                                                                                                                                                                                                  TRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFR
                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sepsis; acne; Sjogren's disease; scleroderma; human; HOTTL.
                                                 Length 362;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                           PWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292
                                                 57.5%; Score 897; DB 3;
57.5%; Pred. No. 4.2e-88;
                                                                                 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HOTTL protein sequence SegID2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ93455 standard; protein; 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feder JN, Wu S, Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                 Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-099381/10.
                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO2004005487-A2.
                  Sequence 362 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           270
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                                                                                                                                                                                                                                                                                                                                                                               253
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
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cantingfammatory, anabolic, hypertensive, endocrine-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antipatkinsonian, antiarthritic, antiasthmatic, nortropic, antipatkinsonian, antiarthritic, antiasthmatic, antipatcing as immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin carboxypeptidase activity, a berrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, plumonary disorders, lung cancer, gastrointestinal disorders, or proliferation, reproductive certical disorders, brain cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph fissue. The BGS-42 polypeptide, polymucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alaheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the human control sequence does not appear in the specification but was obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel testis-specific tubulin tyrosine-ligase -like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEGDRNFWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVWKDGKWVVQKYIERPLLIFG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
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Disclosure; SEQ ID NO 5; 343pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 145; Conservative
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), processed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 SVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 TPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 LKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DIDTSADAVED --- LTEAEWEDLTQQYYSLVHGDAFISNS-----RNYFSQCQALLNRIT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 RKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 292
                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Indels 16;
                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 23727; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.8%; Score 636; DB 4; Length 992; 42.8%; Pred. No. 4.3e-59; Live 59; Mismatches 96; Indels ::
                                                                                                                                    Myers EW;
                                                                                                                                   Li PWD,
              23-MAR-2001; 2001WO-US009231.
                                              23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.89
Matches 128; Conservative
                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                 WPI; 2001-656860/75.
N-PSDB; ABL09748.
                                                                                                 (PEKE ) PE CORP NY.
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Search completed: April Job time : 93.4006 secs

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Sequence

Sequence 25605, A Sequence 12196, A Sequence 12194, A Sequence 12194, A Populore 211, Appl Sequence 44, Appl Sequence 449, Appl Sequence 450, Appl Sequence 17994, A Sequence 17994, A Sequence 206, Appl Sequence 1109, Appl Sequence 24, Appl Sequence 16705, Appl Sequence

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118 QALLINRITSVN----PQT-----DIDGLRN----IWIIKPAAKSRGRDIVCMDRVE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 VEDLTEAEWE------DLT-----DLT----QYYSLVHGDAFISNSRNYFSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 VEVKDEGEWDFYWCDVSWLRENFDHTYMDEHVRISHFRNHYELTRKNYMVKNLKRFRKOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 439;
US-10-204-639-19
US-11-096-568A-12196
US-11-096-568A-12194
US-11-096-568A-12194
US-11-096-568A-12194
US-11-096-568A-12194
US-11-031-206-188
US-11-031-206-188
US-11-130-821-4
US-11-124-367A-449
US-11-124-367A-449
US-11-124-367A-451
US-11-099-658A-17994
US-11-099-658A-17994
US-11-099-658A-17994
US-11-099-658A-17994
US-11-099-658A-17994
US-11-099-658A-17994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 280.5; DB 7;
25.0%; Pred. No. 4.6e-16;
live 65; Mismatches 135;
                                                                                                                                                                                                                                                                       US-11-096-568A-16705
                                                                                                                                                                                                                                         JS-11-080-991-54
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APPLICANI: TAKE, KLIAKO, ICHIRO
APPLICANI: SEKI, NACHIKO
APPLICANI: SCENIKAMA, TSUTOMU
APPLICANI: OYGHIKAMA, TSUTOMU
APPLICANI: OYGHIKAMA, MOTOVUKI
APPLICANI: NACHARI, KENJI
APPLICANI: NACHARI, KENJI
APPLICANI: NACHONI VI SEGUI
TILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATCHING OATE: 201-11-05
NUMBER OF SEQ ID NOS: 4396
LENGTH: 439
                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-11-072-512-3658
Sequence 3658, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOCAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOYO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
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 761
3111
550
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690
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897
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1166
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282
8282
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; ORGANISM: Homo sapiens
US-11-072-512-3658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 101; Conserv
 APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 3371, Ap
Sequence 663, App
Sequence 668, App
Sequence 18, App
Sequence 2246, App
Sequence 2246, App
Sequence 2246, App
Sequence 2505, App
Sequence 2505, App
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Sequence 442, App
Sequence 441, App
Sequence 441, App
Sequence 661, App
Sequence 5799, Ap
Sequence 27769, Ap
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21828, A
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2, Appli
                                                                                          April 4, 2006, 12:59:01; Search time 12.0669 Seconds (without alignments) 1364.812 Million cell updates/sec
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1: /SIDS5/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
3: /SIDS5/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
8: /SIDS5/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
8: /SIDS5/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-072-512-3371

US-10-072-512-3371

US-10-330-773-668

US-10-649-591-18

US-11-072-512-246

US-11-072-512-246

US-11-072-512-2246

US-11-072-512-2246

US-11-072-512-2555

US-11-072-512-2555

US-11-072-512-2565

US-11-072-512-2565

US-11-124-367A-444

US-11-124-367A-444

US-11-124-367A-443

US-11-124-367A-443

US-11-124-367A-441

US-10-095-568A-24769

US-11-096-568A-24769

US-11-095-568A-24769

US-11-095-568A-24769
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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seq length: 200000000
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2854
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Match
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Maximum DB
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117 124

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60 CKVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 L--RMBEFFPETYRLDLKHEREAFFTLFDETQIWICKPTASNOGKGIFLLRNOEEVAALO 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 A----ADHPLSRDNKW-----VVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TSPGYLRPORV 205
                                                                                                                                                                                    283 VIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSP--TMHPST 340
                                                                                                                                                                                                                           340 LLWKKIHRMVILTILAIAPSVPFAANCFELFGFDILIDDNLKFWLLEVNYSPALTLDCST 399
                                                                232 DSAIHLCNNAVQK-----YLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVW---GS 282
233 -FDDMYIVQKYISNPLLIGRYKCDLRIYVCVTGFKPLTIYVYQEGLVRFATEKFDLSNLQ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAK-----LRGLPGQLVDIA
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                                                                                                                          292 NNYAHLTNSSINKSGASYEKIKEVIGHG-----CKWTLSRFFSYLRS-----WDVDDL
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3621, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
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Best Local Similarity 25.5%;
Matches 82; Conservative 3.
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OTSUKI, TETSUJI
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YAMAMOTO, JUN-ICHI
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SATO, HIROYUKI
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NAGAI, KEIICHI
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HIO, YURI
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US-11-072-512-3621
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                                                                                                                                                                                                                                                                                                                                                                                   400 DV 401
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ORGANISM:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 IEINSSPTMHPSTPVTAQLCAQVQEDTIKVA-----VDRSCDIGNFELLWRQPVVE--- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 LEVNASPSLTASSQEDYELKTCLLEDTLHVVDMEARLTGREKRVGGFDLMWNDGFVSREE 397
         :: :: | |: | :: | |: | |: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:
                                                                                                                                                                                                                              214 YKESYLRFSTORFSLDKLDSAIHLCNNAVOKYLKNDVGRSPLLPAHN-----MWTSTRFQ 268
                                                                                                                                                                                                                                                                                                                                                         269 EYL-QRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWL 327
                                                                                                    BILBLAAADHPLSRDNK------WVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWF 213
                                                                                                                                                                                                                                                                            Gaps
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; Pred. No. 4.1e-15;
43; Mismatches 80
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APPLICANT: SEKI, NACHIKO,
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NACHARI, KENJI
APPLICANT: NAGHARI, KENJI
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATCHING UNC: 2.1
SERCIT DEBOTH: 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3371, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
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Best Local Similarity 29.8%;
Matches 72; Conservative 4:
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NAGAI, KEIICHI
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US-11-072-512-3371
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APPLICANT:
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LENGTH: 402
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                   323 HGYARLTLSLYDPHSSDLGGHLTNQFMQK------KSPLYMLLKEHTVWSMEHLNRYIS 375
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216 ESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSP---LLPAHNMWTSTRFQEYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 STRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDF
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                                                                                                                                                                                  Sequence 663, Application US/10330773
FUBLication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
FAPPLICANT: Marc Malandro
TITLE OF INVENTION: NOVAL COMPOSITIONS and Methods in Cancer
CURRENT APPLICANTON NOVAL COMPOSITIONS
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 663
LENGTH: 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 668, Application US/10330773
; Publication No. US2006004026241
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REPRENCE: 529452001300
; CURRENT APPLICATION UNMERR: US/10/330,773
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 797;
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Best Local Similarity 25.4%; Pred. No. 0.013;
                                                                  ---- OROGRGAVWGSVIYPSMK 289
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376 DTFWKARGLAKDW---VFTTLK 394
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US-10-330-773-668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 AHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQE 352
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                                                                                                                                                                                         263 ISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRD
                                                                                                                                                                                                                                         303 SATRFATSL------GSAFHP----VLPHYATV-----PRP-----LNKN
                                                                                                                                                                                                                                                                                                                                                                                                                      380 PPFSGSDLCVAGVSVRRARRQVLPVC-----NLKASASILDA----QPLKARGP
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                                                                                                                                            Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
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                                                                                                 Length 713;
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                                                                                                                                            89;
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24.2%; Pred. No. 0.24;
tive 35; Mismatches 106;
                                                                                          Query Match
3.8%; Score 108; DB 6;
Best Local Similarity 25.0%; Pred. No. 0.5;
Matches 77; Conservative 30; Mismatches 89
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SQUENCE 18, Application US/10649591

Publication No. US20060035237A1

GENERAL INPORMATION:

TITLE OF INVENTION: METHODS AND COMPOSITIONS ITITLE OF INVENTION: CATECORIZING PATIENTS

FILE REFERENCE: CWRU-P03-003

CURRENT APPLICATION NUMBER: US/10/649,591

CURRENT FILING DATE: 2003-08-26

PRIOR FILING DATE: 2002-08-26

PRIOR FILING DATE: 2002-10-18

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FRAESEQ for Windows Version 4.0

SEC INDO. 18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773-668
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524 ASVPPPPG 531
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; ORGANISM: Homo sapiens
US-10-649-591-18
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Best Local Similarity
Matches 74; Conserv
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338 PSTPVTAQ----LCAQVQEDTIKVAVDRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSV 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 DLGLKEEKGLPLALLAPLRGAAESGGAAQPTR----TKAAGKVELPACPCRHVDSQAP-- 495
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-----PSEQVNSKAPLS 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 QSSQVPEKPRPALLPTPV----SFGSAPPTTYHPPLQSAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 MKVAQDHVEPRKNSFE----LYGADFVLGRDFRPW----
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Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOWU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHRI, KENJI
APPLICANT: MAGAHRI, KENJI
APPLICANT: MAGAHRI, KENJI
TITLE OF INVENTION: Novel full length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2002-01-25
PRIOR PELING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SEQ ID NO 246
LENGTH: 723
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                                                                                         ; Sequence 2246, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
                                                                                                                                                  APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
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NAGAI, KEIICHI
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US-11-072-512-2246
557 TGRGS 561
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US-11-072-512-3151
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Best Local S:
Matches 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 ELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPP---- 536
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298 AAPCPPLPAFPALLPAAPCRA----LLPLCAYGAGEPA---RLGAREAEVPPTAPPLLLA 350
                                                                                 351 PLPAAA----PAKPLRGPAAGGAHL-YCPLR--------PAALQAALVRRPGPHLSY 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 PWLIEINS---SPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLWRQPVVEPPP 381
                                                         458 PLRGAAESGGAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVA-QPAKSWDPNQLNAH 516
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3.6%; Score 103; DB 7; Length 710;
Best Local Similarity 23.7%; Pred. No. 1.3;
Matches 58; Conservative 20; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OTSUKA, WULULULAL
APPLICANT: MAGGHARI, KENLI
APPLICANT: MAGGHARI, KENLI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REPERENCE: 084335-0131
CURRENT PELING DATE: 2005-03-07
RRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALCHIN VEY. 2.1
SEQ ID NO 3402
LENGTH: 10
                                                                                                                                                                                                                                                        3-11-072-512-3402
Sequence 3402, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOVUKI
                                                                                                                                                                                                                                                                                                                                      APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3402
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APPLICANT:
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APPLICANT:
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Gaps

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115 SQCQALLNRITSVNP-----QTDIDGLRNIW-----IIK---PAAKSRGRD 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --------DFRPWLIE-----1NSSPTWHPSTPVTAQLCAQVQEDTI-- 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 -SLLNSFHPHEEDLSSISATPLPEEFELQGFLALRPSFRNLDFSKGHQGITGDKEGQQRR 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 ALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKVELPACPCRHV--DSQAP 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 LDSAIHLCNNAVQKYLKNDVGRSPLLPAHNM---WTSTR---FQEYLQRQGRGAVWGSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 MSFLGILCKCPLQNESQEESYNAYPLPAVKVSMDWLRLRPRVFQBAVVDE-RQYIWPWLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 -----LICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
3.5%; Score 100; DB 7; Length 756;
Best Local Similarity 20.2%; Pred. No. 2.6;
Matches 127; Conservative 71; Mismatches 230; Indels 200;
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                       APPLICANT: OTSUKA, MOTOYUKI

APPLICANT: NACHARI, KENJI

APPLICANT: NACHARI, KENJI

APPLICANT: NACHARI, KENJI

APPLICANT: NACHO, YASUHIKO

TITLE OF INVENTION: NOVEL full length cDNA

FILE REFERENCE: 084335-0191

CURRENT APPLICATION NUMBER: US 60/350,978

PRIOR PILING DATE: 2002-01-25

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 2505

LENGTH: 756
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US-11-000-463-375
; Sequence 375, Application US/11000463
; Publication No. US20050266433A1
       YOSHIKAWA, TSUTOMU
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                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
US-11-072-512-2505
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Best Local Similarity
       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 OPLKARGPSAMPDPAQ-----GPPSPALQRDIGLKEEKGLPLALLAPLRGAAESG-- 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 RCROARSPRSSSTISRCTWERTRSTPPGFTAWKTSSARSAVSTPAAACECSRSSPTSWTT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 ----GAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDP--NQLNAHPLE 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 3.5%; Score 100; DB 7; Length 354; l Similarity 26.2%; Pred. No. 0.88; 53; Conservative 23; Mismatches 98; Indels
                                                                                                  APPLICANT: ADDIT, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YURI
APPLICANT: HOO, YURI
APPLICANT: MAGAI, KEIICHI
APPLICANT: RIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: OTSUKA, MODIKUI
APPLICANT: WAGAHARI, KENJI
APPLICANT: MAGHO, YASUHIKO
ITILE OF INVENTION: NOVE! Full length CDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2005-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ 1D NOS: 4096
SOFTWARE: PRED
TYPE: PRT
CORGANISM: HOMO SAPIENE
CONTANTA
CORGANISM: HOMO SAPIENE
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Publication No. US20060029945A1
GENERAL INFORMATION:
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                        WAKAWATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAWOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
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OTSUKA, KAORU
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Best Local Similarity
Matches 53; Conserv
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Section Section

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Sequence 6, Application US/11075185
Publication No. US20050266434A1
GENERAL INFORMATION:
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Best Local Similarity 20.49
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AIHLCNNAVQKYLKNDVGRSPLLPAH-----NMWTSTRFQEYLQRQGRGAVWGSVIYPSM 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 CNLKASASLLDAQPLKARGPSAMP----DPAQ----GP--PSPALQRDLGLKEEKGLP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 LALLAP-----LRGAAESGGAAQPTRTKAAGKV---ELPA----CPCRHVDSQ-APNTGV 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 KKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRP----WLIEINSSPTMHPSTPVTA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 --CLAPADTEQODHTSPNEN-----DQVTPQHREPAGPNTQIRSGSAP---PATPVMV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 QLCAQVQEDTIKVAVDRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QKYIETPLLICDIKFDIRQWFLVTD----WNPLTIWFY---KESYLRFSTQRFSLDKLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ILINKLEFYCHPYFQRD---SPHLLVRMKRRVGVKSAPRHQEEDKPEAAGS------
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3.5%; Score 99.5; DB 7; Length 423;
Best Local Similarity 24.4%; Pred. No. 1.3;
Matches 89; Conservative 34; Mismatches 125; Indels 117;
                                                                                                          APPLICANT: Wang, Aladonoug b.
APPLICANT: Wang, Zilwei
APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION NUMBER: US/11/000,463
CURRENT APPLICATION NUMBER: US/21,265
FRIOR APPLICATION NUMBER: 10/291,265
FRIOR APPLICATION NUMBER: PCT/US01/02623
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR APPLICATION NUMBER: 09/491,404
FRIOR FILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: 09/617,746
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2000-09-15
NUMBER: OF SEQ ID NOS: 944
SEQ ID NO 375
FRIOR FILING DATE: 2000-09-15
NUMBER: FastSEQ EOr Windows Version 3.0
                                                                               Chen, Rui-hong
Qian, Xiaohong
                            Tang, Y Tom
Liu, Chenghua
                                                              Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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1448 IGELGRHVAKHLV-----TAHGVRHLVLTSRRGMDAPDAAALVDELRAAGAATVDVA-- 1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1154 OSLARLSREEAAAGDPVLVPFAWTDVALYATGATELRARIALEQAEG---GAPAVASLLL 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 DFVLGRDFRPWLIEINSSPTWH------PSTPVTAQLCAQVQ---EDTIKVAVD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 HGDAFISNSRNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEE 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 ----GQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDL------TQQYYSLV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 NPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTR 266
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APPLICANT: JULIEN, BRYAN
APPLICANT: JULIEN, BRYAN
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REFERENCE: 010099.03
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR PRIOR PRIOR NUMBER: US 60/568,290
PRIOR PRIOR DATE: 2004-03-08
PRIOR PLING DATE: 2004-03-08
PRIOR PLING DATE: 2004-03-08
PRIOR PLING DATE: 2004-03-08
PRIOR PLING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR PLING DATE: 2004-03-08
PRIOR PLING DATE: 2004-03-08
PRIOR PLING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR PLING DATE: 2004-03-08
PRIOR PRIOR DATE: 2004-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.5%; Score 99.5; DB 7; Length 1892;
20.4%; Pred. No. 11;
tive 70; Mismatches 221; Indels 229;
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RESULT 13 US-11-096-568A-21828

RESULT 12 US-11-075-185-6

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1647 -----VQEWQETSPTREEPAGEQKELAPAWEDT-----SPEQDNRYWRGREDVALEQDTY 1696
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                                                                                                                                                                                -----ALLNRITSVNPQTDIDGLRNIWIIKPAAKS-----RGRDI
                                                                                                                                                                                                                                                                                                                                                                                                   206 WNPLT----IWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKY-----LKND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 FELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 LLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLK------ASASLLDAQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 KARG---PSAMPDPAQGPPSPALQR-----DLGLKEEKGLPLALLAPLRGAAE-SGGAA
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                                                                                                                                                                                                                                                                                        154 VCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQW-----FLVTD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1746 ATRSP-----WASD-FKDFQES------
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ORGANISM: Homo sapiens
US-11-124-367A-442
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                                                                           APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PW2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21828
LENGTH: 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 RQVLPVCNLKASASLLDAQPLKAR--GPSAMPDPAQGPPSP---ALQRDLGLKEEKGLPL 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 ALLAPLRGAAESGGAAQPTRTKAAGKVELPACPCRHVDSQ------APNTGVPVAQP 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 GSGASRPGSCSSRGSTGPRRWPAAGGRWRTPCPCASPSPRRARPTAAGGATSTGCSTATA 150
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i Sequence 444, Application US/11124367A

j Publication No. US20060024700A1

j GENERAL INFORMATION:
 APPLICANT: Michaele Cargill

j APPLICANT: Michaele Cargill

j APPLICANT: Hongjin Huang

j TILE OF INVENTION: Genetic Polymorphisms Associated with

TILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

FILE REFERENCE: CL001519.ORD

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT FILING DATE: 2004-05-07

PRIOR APPLICATION NUMBER: US 60/568,846

PRIOR PILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-06-05

PRIOR FILING DATE: 2004-06-05

PRIOR FILING DATE: 2004-06-05

PRIOR FILING DATE: 2004-06-05

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Score 98.5; DB 7; Length 386;
25.5%; Pred. No. 1.3;
tive 14; Mismatches 68; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc feature
; LOCATION: (1). . (386)
; OTHER INFORMATION: Ceres Seq. ID no. 12406424
US-11-096-568A-21828
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SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 21828, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.5*
Matches 47; Conservative
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ORGANISM: Homo sapiens
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151 ARTW 154
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24 RDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIACKVCQAYLGQLEHEDIDTS 78 : :	79 ADAVEDLITEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQ 118	119RGRDI 153 	154 VCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTD 205 	206 WNPLTIMFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKUD 249 1 1697 WRELSCERKVWFPHELDGQGARPHYTERRESTFLDEGPDDEQEVPLREH 1745	250 VGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNS 309	310 FELYGADFVLGRDFRPWLJEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFE 369	370 LLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPL 419 ::	420 KARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAE-SGGAA 469 	470 QPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPA-KSWDPNQLNAHPLE 519 	520 PVLRGLKTAEGALRPPGGKG 540
24 RD(:- 467 KD)	79 AD.	119 587 ED	154 VCI	206 WN 697 WR	250 VG	310 FE 1766	370 LL :: 795 II	420 KA 846 VP	470 QP 903 SP	520 P- 1956 PT
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Search completed: April 4, 2006, 12:59:34 Job time : 13.0669 secs

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Biocceleration Ltd.
 GenCore version
Copyright (c) 1993 - 2006
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- protein search, using sw model OM protein

4, 2006, 12:55:16; Search time 77.9122 Seconds (without alignments) 2900.544 Million cell updates/sec April Run on:

Perfect score:

US-10-635-977-2 2854 1 MASSILKWVVSHQSCSRSSR......LRGLKTAEGALRPPPGGKGS Sequence:

541

Scoring table:

1867569 seqs, 417829326 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Sequence 2, Appli	7	13	13,	14,	14,	4	4	Ŋ	617	617		7	25		5, Apr					190	. 26,	26,	5184	205823	8	Sequence 8, Appli
SUMMARIES	ID	US-10-615-659-2	US-10-635-977-2	US-10-615-659-13	US-10-635-977-13	US-10-615-659-14	US-10-635-977-14	US-10-615-659-4	US-10-635-977-4	US-10-275-595A-5	US-09-925-298-617	US-10-102-806-617	US-10-615-659-7	US-10-635-977-7	US-10-756-149-5267	US-10-108-260A-4209	US-10-615-659-5	US-10-635-977-5	US-11-097-143-23727	US-11-097-143-23415	-10	US-11-097-143-19014	US-10-615-659-26	US-10-635-977-26	US-10-756-149-5184	US-10-424-599-205823	US-10-615-659-8	US-10-635-977-8
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de	Query	100.0	100.0	9.66	9.66	54.7	54.7	45.5	45.5	35.5	34.0	34.0	33.5	33.5	33.5	33.1	30.3	30.3	25.3	18.8	13.2	11.5	11.3	11.3	10.6	10.6	10.5	10.5
	Score	2854	2854	2843	2843	1560	1560	1299	1299	1013	969.5	969.5	956.5	956.5	956.5	944.5	865.5	865.5	722.5	536.5	375.5	328	322	322	303.5	302	299.5	299.5
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Seguence 9312, Ap	Sequence 7680, Ap	Sequence 4080, Ap		21,	22,	Sequence 21, Appl	22,	3821		Sequence 21303, A		9	Sequence 262294,	Sequence 118, App	Sequence 1, Appli	Sequence 24, Appl	Sequence 24, Appl
US-11-097-143-9312	US-11-097-143-7680	US-11-097-143-4080	US-10-104-047-3658	US-10-615-659-21	US-10-615-659-22	US-10-635-977-21	US-10-635-977-22	US-09-864-761-38213	US-10-104-047-3371	US-11-097-143-21303	US-10-615-659-6	US-10-635-977-6	US-10-424-599-262294	US-10-210-130-118	US-10-250-613-1	US-10-615-659-24	US-10-635-977-24
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297.5	291	282.5	280.5	274	274	274	274	271.5	271.5	270	259	259	258	254.5	254.5	237	237
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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; Sequence 2, Application US/10615659; Publication No. US20040157234A1; General INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company; TITLE OF INVENTION: TROUNDED ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN; TITLE OF INVENTION: TROSINE-LIGASE-LIKE PROTEIN, BGS42; FILE REFERENCE: DO283 NP; CURRENT APPLICATION NUMBER: US/10/615,659; PRIOR APPLICATION NUMBER: US. 60/394,725; PRIOR APPLICATION NUMBER: US. 60/394,725; NUMBER OF SEQ ID NOS: 102; SOFTWARE: Patentin version 3.2; SOFTWARE: Patentin version 3.2; SEWITH: 541

TYPE: RT
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100.0%; Pred. No. 3.1e-229;
ative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 541; Conservative
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US-10-615-659-2
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Sequence 13, Application US/10615659
; Publication No. US20040157234A1
GENERAL IRPORMATION:
GENERAL IRPORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION NUMBER: US/10/615,659
CURRENT APPLICATION NUMBER: US. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin version 3.2
; ERGIN NO 13
LENGTH: 541
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llarity 99.6%; Pred. No. 2.5e-228;
Conservative 0; Mismatches 2;
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ORGANISM: Homo sapiens
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Query Match
Best Local Similarity 100.0
Matches 293; Conservative
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ORGANISM: Homo sapiens
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US-10-635-977-14
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                                                                        Sequence 13, Application US/10635977

Sequence 13, Application US/10635977

Publication No. US20040171131A1

GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: D0283A CIP

CURRENT APPLICATION NUMBER: US/10/635,977

CURRENT FILING DATE: 2003-08-07

PRIOR PILING DATE: 2002-07-09

PRIOR FILING DATE: 2003-07-09

NUMBER: U.S. 10/615,659

PRIOR FILING DATE: 2003-07-09

NUMBER: PARIOR FILING DATE: 2003-07-09

SOFTWARE: PATENTING NUMBER: U.S. 10/615,659

SOFTWARE: PATENTING NUMBER: U.S. 10/615,659

SOFTWARE: PATENTING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SEQ ID NO 13

LEADTH: S41
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Pred. No. 2.5e-228;
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Best Local Similarity 99.6
Matches 539; Conservative
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US-10-635-977-13
541 $ 541
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Sequence 14, Application US/10635977

Publication No. US20040171131A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BG842

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BG842

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BG842

CURRENT FILING DATE: 2003-08-07

PRIOR FILING DATE: 2003-08-07

PRIOR FILING DATE: 2002-07-09

PRIOR PILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SSOFTWARE: Patentin version 3.2

LENGTH: 293
Sequence 14, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
FAPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: DO233 NP
CURRENT APPLICATION NUMBER: US/10/615,659
FRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR PILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.2
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100.0%; Pred. No. 1.5e-121
iive 0; Mismatches 0;
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Matches 293; Conservative
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Sec. 180

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TYPE: PRT ORGANISM: Homo sapiens
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYPOSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: D0283 NP
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR PILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTMARE: Patentin version 3.2
SOFTMARE: Patentin version 3.2
SEQ ID NO 4
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; Sequence 4, Application US/10635977
; Publication No. US20040171131A1
; GENERAL INFORMATION:
, APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
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                                                                   61 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 120
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Publication No. US20040157234A1
GENERAL INFORMATION:
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US-10-615-659-4
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Best Local S
Matches 242
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313 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLW 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IDGLENIWIIKPARKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVXXIETPLLICD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
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APPLICANT: LAL, Preeti
APPLICANT: YAO, Monique G.
APPLICANT: BANDMAN, Olga
APPLICANT: BATRA, Sajeev
APPLICANT: KEARNEY, Lian
APPLICANT: KEARNEY, Lian
APPLICANT: COLICKY, Jennifer L.
TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
FILE REFERENCE: PF-0772 USN
; TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS; FILE REPERENCE: D0283A CIP; CURRENT APPLICATION NUMBER: US/10/635,977; CURRENT FILING DATE: 2003-08-07; PRIOR APPLICATION NUMBER: U.S. 60/394,725; PRIOR PILING DATE: 2002-07-09; PRIOR PILING DATE: 2003-07-09; PRIOR PILING DATE: 2003-07-09; NUMBER OF SEQ ID NOS: 103; SOFTWARE: Patentin version 3.2; SEQ ID NO 4.5; SEQ ID NO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/275,595A CURRENT FILING DATE: 2003-06-13
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PRIOR APPLICATION NUMBER: US 60/201,960
PRIOR FILING DATE: 2000-05-05
PRIOR PLILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-05-08
PRIOR PELICATION NUMBER: US 60/209,705
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
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APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
APPLICANT: BU-Dyung Aina M.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: AZIMZAL, Yalda
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: BUNFORD, Neil
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233 348

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49 RGLPGQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFIS 108
                                                                                                                                                                                         109 NSRNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAA 168
                                                                                                                                                                                                            54 HLDTQVQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNG 113
                                                                                                                                                                                                                                                                                         . LOCATION: (307)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-102-806-617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 RGLPGQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFIS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 NSRNYFSOCOALLNRITSVNPOTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAA 168
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                                                                                                                                            9 RGVPYQ------LGPHGHRQ---GLEAPLYLTPEGWSLFLQRYYQVVHEGAELR
                                                                                                                                                                                                                                                                                                                                         229 DKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRGGRGAVWGSVIYPSM
                                                                                                                                                                                                                                                                                                                                                                   289 KKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCA
                                                                                                                                                                                                                                                                169 DHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 QVQEDTIKVAV----DRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 GVQADTLKVVIDRXLDRNCDTGAFELIYKQPAVEVPQYVGIRLLVBGFTIKK 345
                                                                                  19;
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                                                Length 362;
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FILE REFERENCE: PALOSPIC.
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 617
                                                                                  Indels
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52.0%; Pred. No. 4.1e-72;
tive 58; Mismatches 92;
                                              DB 3;
                                          34.0%; Score 969.5; DB 3 52.0%; Pred. No. 4.1e-72; ative 58; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 617, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
                                        Query Match
Best Local Similarity 52.0%
Matches 183; Conservative
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Best Local Similarity 52.0%
Matches 183; Conservative
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ORGANISM: Homo sapiens
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       US-09-925-298-617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAQG--PPSPAL-QRDLGLKEEKGLPLALLAPLR--GAAESGGAAQP---TRTKAAGK-- 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (307)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 LIMROPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLKARGPSAMPD 429
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1S-09-925-298-617
Sequence 617, Application US/09925298
Sequence 617, Application US/09925298
Publication No. US20020039764A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
                                                                                                                                                                                                                           Length 488;
                                                                                                                                                                                                                                                              68; Mismatches 138; Indels
                                                                                                                                                                                                                          35.5%; Score 1013; DB 4; 45.5%; Pred. No. 1.5e-75;
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OTHER INFORMATION: Incyte ID No: 2156553CD1
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PERL PROGram
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Matches 214; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 617
LENGTH: 362
                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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                                                                             LENGTH: 488
                                                      SEQ ID NO 5
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APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITI
TITLE OF INVENTION: METHODS OF SCREENING, FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: Patentin version 3.2
SEQ ID NO 5267
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICUT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNFE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 DIDTSADAVEDLITEAEWEDLIQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLL PAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
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54.2%; Pred. No. 4.8e-71;
iive 55; Mismatches 91
                                                                                                                                                                                                                                                                                           Query Match 33.5%; Score 956.5; DB 4 Best Local Similarity 54.2%; Pred. No. 4.8e-71; Matches 179; Conservative 55; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLWROPVVEPPFSGSDLCVAGV-SVRRAR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FILE REFERENCE: D0283A CIP; CURRENT APPLICATION NUMBER: US/10/635,977
; CURRENT FILING DATE: 2003-08-07; PRIOR APPLICATION NUMBER: U.S. 60/394,725; PRIOR FILING DATE: 2002-07-09; PRIOR FILING DATE: 2002-07-09; PRIOR FILING DATE: 2003-07-09; NUMBER: OF SEQ ID NOS: 103; SEQ ID NO S: 103; SEQ ID NO IN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5267, Application US/10756149; Publication No. US20050181375A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.59
Best Local Similarity 54.29
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo Sapiens
US-10-756-149-5267
                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-756-149-5267
                                                                                                                                                                                                  LENGTH: 352
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ORGANISM:
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Publication No. US20040157234A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REPERENCE: DO283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT PILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR APPLICATION NUMBER: U.S. 60/394,725
SPOID NOS: 102
SOFTWARE: Patentin version 3.2
SEQID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10635977
Publication No. US20040171131A1
GENERAL INFORMATION:
APPLICANT: BISTON:
APPLICANT: BISTON-Hyers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 GADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRMLDRNCDTGAFE 301
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                                                                                                                         KKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCA 348
      114 NPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIDKDLEAPLYLTPEGWSLFLORYYOVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGLRNIWIIKPAAKSRGRDIVCMDRVEBILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                            DKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSM
                                                                    74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
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                                                                                                                                                                                                                          294 GVQADTLKVVIDRXLDRNCDTGAFELIYKQPAVEVPQYVGIRLLVVEGFTIKK 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 LLWROPVVEPPPSGSDLCVAGV-SVRRAR 398
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ORGANISM: Homo sapiens
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COMPOSITIONS AN

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PLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY 313
                                                              74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIBTPLLICDT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGABLRHLDTQVQRCEDILQQLQAVVPQIDM 61
                                                KFDIROWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVOKYLKNDVGRS
                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                        Sequence 4209, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFRENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT PILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOUTHWARE: Patentin Ver. 2.1

SEQ ID NO 4209
                                                                                                                                                                                                                        370 LLWROPVVEPPFSGSDLCVAGV-SVRRAR 398
                                                                                                                                                                                                                                            302 LIYKQPVITSPASTPRPSCLLPMYSDTRAR 331
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Job time : 78.9322 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4209
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RESULT 1
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(Ggn2_6/ptodata/1/iaa/5_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/6_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/H_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/RE_COMB.pep:*

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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
SUMMARIES	ID	US-10-104-047-3658	US-10-104-047-3371	US-09-270-767-46703	US-10-104-047-3621	US-09-270-767-62411	US-09-270-767-46787	US-09-248-796A-14603	US-09-538-092-31	US-09-270-767-46577	US-09-252-991A-16967	US-09-823-240A-2	5208144-8	US-09-949-016-6778	US-09-949-016-11687	US-09-252-991A-25927	US-08-290-731C-2	US-08-290-731C-6	US-09-491-356C-9	US-09-902-540-14992	US-09-252-991A-25999	US-09-252-991A-17140	US-10-002-344A-237	US-09-134-001C-3530	US-09-252-991A-17729	US-09-270-767-45812	US-09-252-991A-18857	US-09-252-991A-32892
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	Score	280.5	271.5	212	183	154.5	154.5	151	144.5	126	126	125.5	123	120	120	120	114.5	114.5	113.5	111	110.5	107.5	107	107	106.5	106.5	106	106
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Sequence 32139, A	Sequence 31760, A	Sequence 32660, A	Sequence 23080, A	Sequence 9170, Ap	Sequence 3, Appli	Sequence 3, Appli	186	Sequence 8369, Ap	Sequence 21872, A	Sequence 8, Appli	Sequence 7, Appli	9	Sequence 20033, A		Sequence 159, App	Sequence 3402, Ap	Sequence 12305, A
US-09-252-991A-32139	US-09-252-991A-31760	US-09-252-991A-32660	US-09-252-991A-23080	US-09-949-016-9170	US-08-906-865-3	US-09-129-668-3	US-09-252-991A-18696	US-09-949-016-8369	US-09-252-991A-21872	US-09-150-460B-8	US-09-150-460B-7	US-09-150-460B-6	US-09-252-991A-20033	US-09-252-991A-32630	US-09-758-759-159	US-10-104-047-3402	US-09-902-540-12305
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3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
105.5	105.5	105	105	105	104.5	104.5	104	104	103.5	103.5	103.5	103.5	103	103	103	103	102.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

18; 82 VEDLTEAEWE------DLT------QQYYSLVHGDAFISNSRNYFSQC 117 124 118 QALLNRITSVN----PQT------DIDGLRN----IWIIKPAAKSRGRDIVCMDRVE 160 268 EILELAAADHPLSRDNK------WVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWF 213 237 FAECLLWSGHRR------ODVHLTNVAVOK------TSPDYHPKKGCKWTLQRFR 279 EYL-OROGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWL 327 328 IEINSSPIMHPSTPVTAQLCAQVQEDTIKVA-----VDRSCDIGNFELLWRQPVVE--- 378 :|:|:||:: |: :| : | 338 LEVNASPSLTASSQEDYELKTCLLEDTLHVVDMBARLTGREKRVGGFDLMMNDGPVSREE 397 65 VEVKDEGEWDFYWCDVSWLRENFDHTYMDEHVRISHFRNHYELTRKNYMVKNLKRFRKQL 214 YKESYLRFSTORFSLDKLDSAIHLCNNAVOKYLKNDVGRSPLLPAHN-----MWTSTRFQ Indels 103; Length 439; Sequence 3658, Application US/10104047

Patent No. 6942241

GENERAL INFORMATION:
APPLICANT HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REPREBRICE: H1-ADIOS
CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT PILING DATE:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SEQ ID NO 3658
LIENGTH: 439 Query Match 9.8%; Score 280.5; DB 2; Best Local Similarity 25.0%; Pred. No. 3e-18; Matches 101; Conservative 65; Mismatches 135; TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-3658 161 269 ద ð 유 g 셤 셤 ò 셤 ð ઠ ò ઠે

379 -PPPFSGSDLCVAGVSV-----RRARRQVLPVCNL----KASA 411

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376 DTFWKARGLAKDW---VFTTLK 394
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                                                                                                                                                                     341 PVTAQLCAQVQEDTI 355
                                                                                                                                                                                                         173 PLDTKVKSCLMADLL 187
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CORGANISM: Homo sapiens
US-10-104-047-3621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 DSAIHLCNNAVQK-----YLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVW---GS 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 YFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 SRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKL- 231
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Sequence 46703, Application US/09270767

Barent No. 6703491

GENERAL INFORMATION:
APPLICANTINE Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6703
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 271.5; DB 2; Length 592;
; Pred. No. 3.6e-17;
43; Mismatches 80; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 212; DB 2; Length 561;
29.2%; Pred. No. 1.9e-11;
tive 37; Mismatches 75; Indels
398 GAPDLSGMGNFVTNTHLGCVNDRKKQLRQLF--CSLQVQKKASS 439
                                                                                                                              GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT PLING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
SRIOR APPLICATION NUMBER:
SRIOR APPLICATION NUMBER:
SRIOR RILING DATE:
SOFTWARE: PatentIn Ver. 2.1
SSQ ID NO 3371
LENGTH: 592
                                                                                          Sequence 3371, Application US/10104047 Patent No. 6943241
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US-09-270-767-46703
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Best Local Similarity 29.84
Matches 72; Conservative
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US-10-104-047-3371
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Best Local Similarity
Matches 57; Conserv
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119 LKW-----CEVKSRDSYGSFRE--GEQLLYQLPNNKLLTTKIGLLSTLRG-RARAMSRA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 AKTRSMEDDPIHHKTPFRGPQARVVQRYIQNPLLVDGRKFDVRSYLLIACTTFYMI-FFG 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 CKVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 ESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSP---LLPAHNMWTSTRFQEYL- 271
                                                     61 HICHYSINKYHSDYIRSSDAQDEDVG------HKWTLSALLRHLKLQSCDTRQLMLNI 112
                                                                                                                                                  -SVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPST 340
                                                                                                                                                                                                ---DVGRSPLLPAHNMWTSTRFQEYLQRQG---RGAVWG- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62411, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REPRENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKVPGGVQARLEK---DAAAPALEDL---PW-------TSPGYLRPQRV
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Best Local Similarity 25.5%; Pred. No. 7.3e-09;
Matches 82; Conservative 38; Mismatches 118; Indels
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION ON. 6943241el full length cDNA
TITLE OF INVENTION: NO. 6943241el full length cDNA
TITLE OF INVENTION: NO. 6943241el full length cDNA
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
HIGH DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
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80 SQLRHFIVQEYKSNPLLL--SKYDHKKFHLRTYVVCVGDLKVFVYKNVLTLFAGEPYKLP 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 ----DKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVI 284
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                                                                                                                                                                                                                                                                                                                                                                                                173 SRDNKWVVQKYIETPLLICDTKFDIROWFL---VTDWNPLTIWFYKESYLRFSTQRFSL-
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APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INFORMATION: Protein Complexes and Method of Using Same
FILE REPERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                Length 259;
                                                                                                                                                                                                                                                              81; Indels
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21.8%; Pred. No. 0.00011;
ive 44; Mismatches 105;
                                                                                                                                                                                                              Query Match 5.3%; Score 151; DB 2; Best Local Similarity 22.6%; Pred. No. 4.4e-06; Matches 53; Conservative 50; Mismatches 81
                                                                                                                                                                                                                                                                                                        132 DIDGLRNIWIIKPAAKSRGRDI---VCMDRVEEIL--
    PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14603
LENGTH: 259
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                                                                                                                                            ORGANISM: Candida albicans
US-09-248-796A-14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 21.89
Matches 57; Conservative
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APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-13
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192 ---GPKIAQKYIERPVLFSRQEVEGSVKFDIRYVILLKSVKPLKAYIHRKFFLRFANHPF 248
                                                                                                                                                                                                                                                                            125 TSVNPQTDI------DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPL 172
                                                                                                                                                                                                                                                                                                                                                                      173 SRDNKWVVQKYIETPLLIC-----DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRF 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46787, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                       136 TTYNLSTEVKEFAAYYOTRAAKGLDNHWIIKPWNLARGLDTHITDNIKQIVRLPAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRDNKWVVQKYIETPLLIC-----DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRF
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                      DB 2;
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Pred. No. 6e-06;
                                                                                                                                                                                  Score 154.5; DB Pred. No. 2e-06;
                                                                                                                                                                                                                                 18; Mismatches
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                                                                                                               ; ORGANISM: Drosophila melanogaster US-09-270-767-62411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Drosophila melanogaster US-09-270-767-46787
                                                                                                                                                                                    5.4%;
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Best Local Similarity 31.7%;
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 62411
LENGTH: 260
                                                                                                                                                                                                                                 40; Conservative
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Matches 40; Conserval
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LENGTH: 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAAGKV------ELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPL 518
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                 ----SADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLN 122
                                                                                                                                          : : : : : | : | 365 PLKQIADTLAVLGFGQPRKVILDQLDVIHALAQGRREPSDAILMDVAGALLYVEATLAGM 424
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                                                             308 DHETVDAERARLAGPDRDAMRSVVGALCEELVRIKDSL---DLFVRSDRGHPSELDALLA 364
                                                                                                                                                                                                                                     | | ::: | | :: | 425 AGPGDERNSESSRLPTTDVAQIHQLVIKEARNGLEQAKDAIIBFIASQWNHEHLARVPEL
                                                                                                                                                                                                                                                                                                     217 -SYLRFSTORFSLDKLDSAIHLCNNAVOKYLKNDVGRSPLLPAHNMWTS-----TRF
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                                                                                                            ---LRNIWIIKPAAKSRGR--DIVCMDRVEEILELAA----
                                                                                                                                                                                                       168 ---ADHPLSRDNKWVVQKYIET-PLLICDTKFBIRQ-----WFLVTDWNPLTIWFYKE-
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; Sequence 2, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
    APPLICANT: Prank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureio
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Methods and Products
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M00656.70064.US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; RIOR APPLICATION NUMBER: 60/194,564
; RIOR PILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; IBENGTH: 802
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Best Local Similarity 24./*
---- 78; Conservative
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US-09-823-240A-2
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US-09-823-240A-2
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Sequence 16967, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
RAPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 NNAVOKYLKUDVGRSPLLPA-----HNMW---TSTRFQEYLORQGR--GAVWGSVI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 AVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMH 337
                           643 NI-KEQIHSITNDVFLAAVNVNRLNFQPLPNAFETYGVDFLIDSNYEVKLLEINAFPDFK 701
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 Y-----PSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTM 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : : | | : : : | | : | HIVRTIIAAKEKDIVNILRSYRTH----NFFDLMRFDLFIDEDLKVFLMEANMSPNL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VQEFVQRPYLVDGHKFDIGVYVVITSVNPLRVYIYTGDVLFRYCPVKYHPFDAEN----
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4.4%; Score 126; DB 2; Length 2482;
Best Local Similarity 19.7%; Pred. No. 0.044;
Matches 122; Conservative 79; Mismatches 207; Indels 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.4%; Score 126; DB 2; Length 305; Best Local Similarity 23.6%; Pred. No. 0.0015; Matches 42; Conservative 36; Mismatches 62; Indels
                                                                                                                                                                                                                                                         Sequence 46577, Application US/09270767 Patent No. 6703491
                                                                                                                        : : : | | : : | | 102 QTGKDLKNLIDELFDDTVKYCV 723
                                                                                             338 PSTPVTAQLCAQVQEDTIKVAV 359
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US-09-252-991A-16967
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US-09-270-767-46577
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LENGTH: 305
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	RESULT 13 US-09-949-016-6778 US-09-949-016-6778 Sequence 6778, Application US/09949016 PARENT NO. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISSASS. METHODS OF DETECTION AND USES THEREOF	Length 542,	Matches 75; Conservative 38; Mismatches 124; Indels 96; Gaps 254 PLLPAHNWTSTRFQEYLQRQGRGAVWGSVIYPSWKKAIAHAMKVAQDHVEFRKNSFELY	Db 233 PLLPGNDVGRSS-YGAMQVKQVFDYAYIVLSHAVSPLARSYPNR 275 Qy 314 GADFVLGRDFRPWLIEINSSPTWHFSTPVTAQLCAQVQEDTIKVAVDRSCD 364	Db 330 TQNREPESPYGGRLTLSLSSPQLLSSGSSASSVSSLSGSDVDSDTPPCTTPSV 382 Qy 410 -SASLLDAQPLKARGPSAMPDPAQEPSPALQRDLGLKEEKGLPLAPLAPLAPARAAE 464 Db 383 YQFSLQAPAPLMAGLPTALPMPS-GKPQPTTSRTLIMTTNNQTRFTIPPPTLGVAPVPCR 441 Qy 465 SGGAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPDAGKSWDPNQLNAHPLEPVLRG 524	Db 442 QAGVEGTASLKAVHHMSSPAIP
Qy 264 STRFQEYLQRQGRGAVWGSVIYPSWKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDF 323 Db 322 ATRFATSL	OY 472TRTKAAGKVELPACPCRHVDSOAPNTGVEVA-OPAKSWDPNOLNAHPLEPV 521 Db 492 SVLPSPSAGAPASAETPLNP-ELGDSSASEPGLQAASQPAESPTPQGLVLGPPAPPPPP 550 Qy 522 LRGLKTAEGALRPPPG 537 Db 551 LPSGPAYASALPPPPG 566	RESULT 12 5208144-8 ; Patent No. 5208144 ; Patent No. 5208144 ; APPLICANT: SMITH, JOHN A.; RAYCHOWDHURY, RAKTIMA; NILES, JOHN L. ; TITLE OF INVENTION: METHOD FOR DETECTION OF HUMAN DNA.; CONTAINING THE GENE ENCODING LOW DENSITY LIPOPROTEIN RECEPTOR. ; NUMBER OF SEQUENCES: 42 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/396,697 ; FILING DATE: 24-MG-1989 ; PRILOR APPLICATION NUMBER: 213,682 ; FILING DATE: 22-FEB-1989 ; FILING DATE: 23-AUG-1988 ; SEQ ID NO:8: ; LENGTH: 884 5208144-8	Query Match 4.3%; Score 123; DB 6; Length 884; Best Local Similarity 19.7%; Pred. No. 0.016; Matches 118; Conservative 69; Mismatches 191; Indels 222; Gaps 31;	Qy 66 YLGQLEH-EDIDTSADAVEDLTEAEWEDLTQQYYS-LVHGDAFISNSRNYFSQCQALLNR 123 Db 328 YLEEEEHIQTIDYDWDPEHIGLSVVYYTVLAQGSQFGAIKBAYIPNFESGSN- 379 Qy 124 ITSVNPQTDID-GLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWV 179 Db 380NPTREVDLGLKYLMOPDGLAVDWVGRHIYMSIN SANSORIEVATLDGRYBRWL 430		298VAQDHVEP

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us-us-cs-syla-csyl, Application US/0925291A
; Sequence 25927, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICATY: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPREBENCE: 10799-02-18
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25927
Sequence 11687, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFREENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-41

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEATSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 PLLPGNDV------GRSS-YGAM---QVKQVPDYAYIVLSHAVSPLARSYPNR 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: ||| |: ||288 DAESTLGRIIKVTQEVIDYRRWIKEKWGSKA-HPSPGMDSRI--KIKE---RIATCNGEQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 TQN-----REP--ESPYGQRLTLSLSSPQLLSSGSSASSVSSLSGSDVDSDTPPCTTPSV 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%; Score 120; DB 2; Length 554; 22.5%; Pred. No. 0.015; tive 38; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 QAGVEGTASLKAVHHMSSPAIP----SASPN---PLSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TAEGALRPPPGGKG 540
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.39,
Best Local Similarity 75,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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                                                                                      361 RSCDIGNFELLWROPVVEPPPF---SGSDLCVAGVSVR------RARRQVLPVCNLKA 409
                                                                                                                                                                               410 SASLLDAQP-----LKARGPSAM-----PDPAQG-----PPSPALQRDLGLK 446
                                                                                                                                                                                                                                                                        447 EEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAK 506
                                                                                                                                728 RTADVS-----ROPLROPPALLORRGDVLDASLAPRPPGFPGAARAKLLLSPACKRGR 781
                                                                                                                                                                                                                         782 ATGLGQRQPGGRGERLSRCPGAATAAGPGGTAHARGPGGGDGLRRRHPPAPARPRGPGLA 841
                                                                                                                                                                                                                                                                                                                     ----PAARROR 869
                                                 Gaps
                                                 78;
Query Match
4.2%; Score 120; DB 2; Length 950;
Best Local Similarity 25.1%; Pred. No. 0.036;
Matches 53; Conservative 17; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                   507 SWDPNQLNAHPLEPVLRGLKTAEGALRPPPG 537
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Search completed: April 4, 2006, 12:46:55 Job time: 22.1171 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 4, 2006, 12:43:06; Search time 81.9545 Seconds (without alignments) 4657.352 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-635-977-2 2854 1 MASSILKWVVSHQSCSRSSR......LRGLKTAEGALRPPPGGKGS 541

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O5jz84 homo sapien		Q8c0v2 mus musculu	mus	29h876 homo sapien	Q8ndn8 homo sapien	26awa3 homo sapien	Q9y4r7 homo sapien	Q4kms8 homo sapien	Q4ry08 tetraodon n	Q922t0 mus musculu	Q58ct2 bos taurus	Q7q156 anopheles g	-	Q7pmd3 anopheles g		Osbhyl drosophila	Ofzu95 homo sapien	Q4v8c1 rattus norv	Q5tnz9 anopheles g			09d570 mus musculu	Q54tul dictyosteli			Q961i9 drosophila	Q9vx74 drosophila			Q7qzc8 giardia lam
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SUMMARIES	ΙD	Q5JZ84 HUMAN	Q8CON7_MOUSE	Q8C0V2_MOUSE	Q8BV51_MOUSE	Q9H876_HUMAN	Q8NDN8 HUMAN	Q6AWA3 HUMAN	TTLL3 HUMAN	Q4KMS8 HUMAN	Q4RY08_TETNG	Q922TO MOUSE	Q58CT2_BOVIN	070156 ANOGA	Q9VM91_DROME	Q7PMD3_ANOGA	Q9VM92 DROME	Q5BHY1_DROME	Q6ZU95_HUMAN	Q4V8C1_RAT	QSTNZ9 ANOGA	Q96GG8_HUMAN	Q641W7_RAT	Q9D570 MOUSE	Q54TU1_DICDI	Q7QTI3_GIALA	Q6BFH6_PARTE	Q96119 DROME	Q9VX74_DROME	Q5VX47_HUMAN	Q4R7H0_MACFA	Q7QZC8_GIALA
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	Query Match Length	747	781	518	704	744	434	352	352	352	534	266	261	572	992	501	719	756	281	375	331	101	461	464	523	1075	794	496	496	341	618	403
46	Query Match	96.0	61.4	60.5	36.9	36.6	34.4	33.5	33.5	33.5	m	29.5	28.3	26.2	25.3	20.5	18.8	18.8	18.4			-	17	12.1	12.1	11.7	11.6	11.5	11.5	11.1	11.1	11.0
	Score	2741	1753.5	1726.5	1052	1043.5	981.5	957.5	956.5	956.5	941.5	834	807.5	746.5	722.5	584.5		\$ 535.5	524.5	524	442.5	385	345.5	345	344.5	335	331.5	328	328	m	315.5	314
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Q6zvt0 homo sapien Q8cfv5 mus musculu Q5t2w4 homo sapien		Veembz nomo sapien Q5r978 pongo pygma Q8r125 mus musculu Q5f498 gallus gall	095922 homo sapien Q91v51 mus musculu Q54384 mus musculu Q5ppi9 rattus norv
Q6ZVTO_HUMAN Q8CFV5_MOUSE O5T2W4_HIMAN	Q8CHB8_MOUSE Q9P1V5_HUMAN Q9UPZ4_HUMAN	QSE978 FONPY QSE125 MOUSE QSF498 CHICK	TTLLI HUMAN TTLLI MOUSE Q54354 MOUSE Q5PPI9_RAT
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311	303.5 303.5 303.5	303.5 303.5 301	298.5 298.5 298.5 298.5
332	35	06644	4 4 4 4 2 60 4 70

ALIGNMENTS

RESULT 1 QSJZ84 HUMAN ID QSJZ84_HUMAN PRELIMINARY; PRT; 747 AA. AC QSJZ84;	Homo sapiens (Human).	Eukaryota, Metazoa, Cnordata, Cranlata, Vertebra Mammalia, Eutheria, Euarchontoqlires, Primates,	Homo NCBI TayID-0606.	[1]	NUCLEOTIDE	Submitted (MAY-2005) to the EMBL/GenBank/DDBJ	EMBL; AL022327; CAI42686.1; -; Genomic_DNA.	GO; GO:0006464; P:protein modification; IBA.	InterPro; IPR004		-		QY 1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60	Db 187 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 246	Gy 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFI 107	Db 247 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVQVPLGSSIVLCIFKIQKVM 306	Qy 108SNSRNYPSQCQALLARITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDR 158	Db 307 MSFEPPTARDRQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRGESPDIVCMDR 364	Qy 159 VEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESY 218	Db 365 VEBILELAAADHPLSRDNKWYVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESY 424	Qy 219 LRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMYTSTRFQEYLQRQGRGA 278	Db 425 IRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNWTSTRFQEYLQRQGRGA 484	CY 279 VWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLJEINSSPTWHP 338	Db 485 VWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHP 544
	DI IV-TWAI-ZUOS (IIEMBLEEL. 30, LABC ANNOCACION Update) GN OTTHUMPRO000028514 (Fragment). GN ORFPARMES-RR93-355C18.2-002;	10-MA1-2005 (TERMBLEEL: 30, LABC ANNOCACION UDGATE) OTTHUMPO000002854 (Fragment) ORFNames-RP3-355C18.2-002; Homo sapiens (Human)	<pre>1.0-mar-2003 (Infembre). OTTHUPP0000028514 (Fragment). ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euvarchontoqlires; Primates;</pre>	10-MA1-2005 (TERBELTEL. 30, LASE ADDOCATION UPDATE) OTTHUMPO0000028514 (Fragment). ORFNames-RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Butheria; Euarchontoglires; Primates; Cata	TO-MAI-ZOUS (ITEMBLEI. 30, LABT ANDOTATION UDGA OTTHUMPROBORDO SETTA (Fragment). ORFNames-RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606;	TO-MAY-2003 (ITEMBLEE). OTTHUPPO0000028514 (Fragment). ORFNames=RP3-355C18.2-002; ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] [1] ONCLEOTIDE SEQUENCE.	TO-MAY-2003 (ITEMBLEEL. 30, LABT ANDOTATION UPOR OTTHINPROBOBOODS 11 (Fragment). ORFNames=RP3-355C18.2-002; ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] (1) (1) (2) (2) (2) (3) (4) (4) (4) (4) (5) (6) (6) (7) (7) (8) (8) (9) (9) (9) (9) (9) (9	OTTHINPOROUGO (ITEMBLEEL. 30, LABT ANDOTATION UPOR OTTHINPOROUGO (ITEMBLEEL. 30, LABT ANDOTATION UPOR OTTHINPOROUGO (2014 (Fragment). ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Matazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euarchontoglires; Primates; Homo. NCB_TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL; ALOS3237; CA142686.1; -; Genomic DNA.	OTTHINPOROUGO (ITEMBLEE). OTTHINPOROUGO (ITEMBLEE). ORFNames=RP3-355C18.2-002; ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] NUCLECTIDE SEQUENCE. Cobiey V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da GO:0004835; P:tubulin-tyrosine ligase activi GO; GO:0004835; P:tubulin-tyrosine ligase activi GO; GO:0004835; P:tubulin-tyrosine ligase activi GO; GO:0006464; P:protein modification; IEA.	OTTHINPOROUGO (ITEMBLEEL. 30, LABE ANDOTATION UPOR OTTHINPOROUGO (ITEMBLEEL. 30, LABE ANDOTATION UPOR OTTHINPOROUGO SELLA (Fragment). ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euarchontoglires; Primates; Homo. NCB_TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL, AL022327; CAI42686.1; -; Genomic_DNA. GO; GO:00044835; F:tubulin-tyrosine ligase activi GO; GO:0006464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase.	OTTHINPOROUGO (ITEMBLEEL. 30, LABT ANDOTATION UPOR OTTHINPOROUGO (ITEMBLEEL. 30, LABT ANDOTATION UPOR OTTHINPOROUGO SELLA (Fragment). ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Matazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] NUCLECTIDE SEQUENCE. Cobiey V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL, AL022327; CA145686.1; -; Genomic DNA. GO; GO:0006464; P:tubulin-tyrosine ligase activi GO; GO:0006464; P:tubulin-tyrosine ligase activi GO; GO:0006464; P:protein modification; IEA. Piam; PF03133; TLL; 1. NON TER.	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Eukaryotas (Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo. NCBL TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CAI42686.1; -; Genomic_DNA. GO, GO:00064835; F: tubulintryrosine ligase activity; IEA. GO; GO:0006445; P: tubulintryrosine ligase activity; IEA. GO; GO:0006446; P: protein modification; IEA. InterPro; IPRO4344; Tub_tyr_lygase. Ffam; PF03133; TTL; 1. NON TER SEQUENCE 747 AA; 83854 MW; F90948EI59BBE589 CRC64; Duery Match SEQUENCE 747 AA; Bassa MW; F90948EI59BBE589 CRC64; Author Match SEQUENCE 747 AA; Bassa MW; F90948EI59BBE589 CRC64; SEQUENCE 747 AA; Bassa MW; F90948EI59BBE589 CRC64;	OTTHUMPO000028544 (Fragment). OTTHUMPO0000028544 (Fragment). ORFNames=RP3-355C18.2-002; Momes=RP3-355C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; (1) NCBI_TaxID=9606; (1) NCBI_TaxID=9606; (1) Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL, AL022327; CA142666.1; -; Genomic_DNA. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0004835; F:tubulin-tyrosine ligase. INCREPTO: IPRO04435; F:tubulin-tyrosine ligase. INCREPTO: IPRO04435; F:tubulin-tyrosine ligase. INCREPTO: IPRO04835; F:tubulin-tyrosine ligase. INCREPTO: IPR	OTTHUMPO000028514 (Fragment). ORFNames=RP3-355C18.2-002; Momes applies (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Momes applies (Human). Eukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae; MCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; ALO22327; CAM120861.; Ganomic_DNA. GO; GO:0004845; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0004464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. Ffam; PF0313; TTL; 1 NON TER SEQÜENCE 747 AA; 83854 MM; F90948EI59BBE589 CRC64; Best Local Similarity 94.0%; Pred. No. 1.1e-181; Matches 529; Conservative 4; Mismatches 6; Indels 24; Gaps I MASSILKWWVSHQSCRSSRSRFRPROREEAGSSDLSSRQDAENMEAKIRGLEGGLVUDIAC 24 187 MASSILKWWVSHQSCRSSRSRFRPROREEAGSSDLSSRQDAENMEAKIRGLEGGLVUDIAC 24	OTTHUMPO000028514 (Fragment). OTTHUMPO0000028514 (Fragment). ORFNames=RP3-355C18.2-002; Momo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae; Momo. NCBL_TaxID=9606; (1) WOLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL, AL022327; Ca142686.1; -; Genomic DNA. GO; GO:0004835; F: tubulin-tyrosine ligase activity; IEA. GO; GO:0004835; F: tubulin-tyrosine ligase. GO:0004836; F: tubulin-tyrosine ligase. GO:0004836; F: tubulin-tyrosine lig	OTTHUMPO0000028514 (Fragment). OTTHUMPO0000028514 (Fragment). ORFNames=RP3-355C18.2-002; Bunkes=RP3-355C18.2-002; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; MCLEOTIDE SEQUENCE. (1) Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; ALO22237; CAM120861.; Genomic_DNA. GO; GO:0004845; F:tubulin-tyrcaine ligase activity; IEA. GO; GO:0004844; Tub_tyr_lygase. InterPro; IRR04444; Tub_tyr_lygase. OO: GO:000464; P:protein modification; IEA. INTERPRO; IRR04444; Tub_tyr_lygase. Ffam; PF0313; TTL; 1. NON_TER SEQUENCE 747 AA; B33854 MW; F90948E159BBE589 CRC64; Query Match 96.0%; Score 2741; DB 2; Length 747; Best Local Similarity 94.0%; Pred. No. 1.1e-181; Matches 529; Conservative 4; Mismatches 6; Indels 24; Gaps IMASSILKWVVSHQSCSRSSRSRPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60	OTTHUMPO0000028514 (Fragment). ORFNames=RP3-355C18.2-002; ORFNames=RP3-355C18.2-002; Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eurrchontoglires; Primates; Catarrhini; Hominidae; Homo. NUCLECTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL02232; CA142686.1; -; Genomic_DNA. GO; GO:0004835; F:tublin-tyxosine ligase activity; IEA. GO; GO:0004835; F:tublin-tyxosine ligase activity; IEA. GO; GO:0004835; F:tublin-tyxosine ligase activity; IEA. GO; GO:0004835; F:tublin-tyyasae. InterPro; IPR004334; Tub_tyr_lygase. PRAM: PF03133; TTL; 1. NON TER. SEQUENCE 747 AA; 83854 MW; F90948E159BE589 CRC64; MACCIA Similarity 94.0%; Pred. No. 1.1e-181; Matches 529; Conservative 4; Mismatches 6; Indels 24; Gaps	OTHINPROBOONORSELY (Fragment). OTHINPROBOONORSELY (Fragment). ORFNAmes=RP3-155C18.2-002; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo. NCBI TaxID=9606; [1] NUCLEOTIDE SEQUENCE. CObley V; NUCLEOTIDE SEQUENCE. CObley V; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; ALO2237; CA142686.1; -; Genomic_DNA. EMBL; ALO2237; CA142686.1; -; Genomic_DNA. GO; GO:0006484; P:Protein modification; IEA. GO; GO:00064835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:00064835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0006484; P:Protein modification; IEA. InterPro; IDR00434; Tub_tyr_lygase. Pfam; PF03133; TTL; 1. NON TER 1	OUTHUMPO00002854 (Fragment). ORRNames=RP9-35518.2-002; Homo sapiens (Human). ORRNames=RP9-35518.2-002; Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Bukaryota, Metazoa; Chordata, Craniata; Primates; Catarrhini; Hominidae; Homo. NCB_TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Farabulin-tyrosine ligase activity; IEA. Go; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:004835; F:tubulin-tyrosine ligase. INNON TER 1 SEQUENCE 747 AA; AB; Bas4 MW; F90948E159BEE589 CRC64; Aussiliarity 94.0%; Pred. No. 1.1e-18; MASSILKWVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKIRGLPGQLVDIAC INNON TER 10	OTTHUMPO0000028(1 (Frameworth). OTTHUMPO0000028(1 (Frameworth). DATE ADDRAG (Human). ENARALOGA: Septement). ENARALOGA: Stremeworth (Human). ENARALOGA: Stremeworth (Human). Mammalia; Butheria; Evarchontoglires; Primates; Catarrhini; Hominidae; Homo sapiens (Human). NCBI_TAXID=9606; NON TER SEQÜENCE 747 AA; 83854 MW; F90948E159BBE589 CRC64; DATE: 1 SEQÜENCE 747 AA; 91.04; Dred. 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Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] NUCLEOTIDE SEQUENCE. CObLey V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL; AL022327; CA1420861; -; Genomic DNA.	Homo sapiens (Human) Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; Homo NCBI_TaxID=9606; [1] NUCLBOTIDE SEQUENCE. Cobley V. Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL; AL022327; CAI42686.1; -; Genomic_DNA. GO; GO:0004835; P: tubulin-tyrosine ligase activi GO; GO:0004835; P: tubulin-tyrosine ligase activi GO; GO:0006464; P: protein modification; IEA.	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] NUCLECTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL; ALLO22327; CAH2686.1; -; Genomic_DNA. GO; GO:0004835; F:tubulin-tyrosine ligase activi GO; GO:0004644; P:protein modification; IEA.	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Evarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] NUCLBOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL; AL022327; CAI42686.1; -; Genomic_DNA. GO; GO:00064835; P: tubulin-tyyrosine ligase activi GO; GO:0006464; P: protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. NON TER. NON TER.	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Butheria; Euarchontoglires; Primates; Homo. NCBI_TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ da EMBL; AL022327; CA142686.1; -; Genomic_DNA. GO; GO:0004835; F:tubulin-tyrosine ligase activi GO; GO:0004464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. Pfam; PF03133; TTL; 1. NON_TER. SEQUENCE 747 AA; 83854 MW; F90948EIS9BBES89	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. NUCLEOTIDE SEQUENCE. Cobley V.; Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CAI42686.1; -; Genomic_DNA. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0004644; P:protein modification; IEA. GO; GO:0004644; P:protein modification; IEA. GO; GO:0006464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. Pfam; PF03133; TTL; 1. NON TER SEQUENCE 747 AA; 83854 MW; F90948EI59BBE589 CRC64; Duery Match SEQUENCE 747 AA; Bass MW; F9094BEI59BBE589 CRC64; Auch Match SEQUENCE 747 AA; Bass MW; F9094BEI59BBE589 CRC64; Auch Match SEQUENCE 747 AA; Bass MW; F9094BEI59BBE589 CRC64;	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo NCBI TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL023327; CA142686.1; -; Genomic_DNA. GO; GO:0004885; F:tubblin-tyrosine ligase activity; IEA. GO; GO:0004885; F:tubblin-tyrosine ligase activity; IEA. GO; GO:0004885; F:tubblin-tyrosine ligase. Interpro; IPR004344; Tub_tyr_lygase. Interpro; IPR004344; Tub_tyr_lygase. PRAM: PF03133; TTL; 1. NON TER SEQUENCE 747 AA; 83854 MW; F90948E159BBE589 CRC64; Guery Match Best Local Similarity 94.0%; Pred. No. 1.1e-181; Matches 529; Conservative 4; Mismatches 6; Indels 24; Gaps 1 MASSILKWVVSHQSCSRSSRRRRPDREBAGSSDLSSRQDAENAEAKIRGLPGQLVDIAC 60	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Homo. NGEL TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CA142686.1; -; Genomic_DNA. GO; GO:0004646; P:protein modification; IEA. GO; GO:0004645; P:protein modification; IEA. GO; GO:000444; Tub_tyr_lygase. Pfam; PF03133; TTL; 1. NON TER SEQUENCE 747 AA, 83854 MW; F90948E159BBE589 CRC64; Duery Match 96.0%; Score 2741; DB 2; Length 747; Best Local Similarity 94.0%; Pred. No. 1.1e-181; MASSILKWVVSHOSCRSSRSRSRPRDQREEAGSSDLSSRQDAENARAKIRGLPGQLVDIAC 24 187 MASSILKWVVSHOSCSRSSRSRPRDQREEAGSSDLSSRQDAENARAKIRGLPGQLVDIAC 24	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo. NUCLECTIDE SULPRICE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CA142686.1; -; Genomic_DNA. GO; GO:0004835; F: tubulin-tyrosine ligase activity; IEA. GO; GO:0004843; F: tubulin-tyrosine ligase activity; IEA. GO; GO:0004843; F: tubulin-tyrosine ligase activity; IEA. GO; GO:0004844; P: protein modification; IEA. InterPro; IPR04344; Tub_tyr_lygase. PRAM: PF03133; TTL; 1. NON TER. SEQUENCE 747 AA; B3854 MW; F90948E159BE589 CRC64; Best Local Similarity 94.0%; Pred. No. 1.1e-181; Matches 529; Conservative 4; Mismatches 6; Indels 24; Gaps I	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae; Homo. [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CA142686.1; -; Genomic_DNA. GO; GO:0004645; P:protein modification; IEA. MON TER SEQUENCE 747 AA, 83854 MW; F90948E159BBE589 CRC64; Deery Match 96.0%; Score 2741; DB 2; Length 747; Best Local Similarity 94.0%; Pred. No. 1.1e-181; MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 24	Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo. NGEL TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL022327; CA142686.1; -; Genomic_DNA. GO; GO:00064835; F:tubblint-tyrosine ligase activity; IEA. GO; GO:0006464; P:protein modification; IEA. GO; GO:0006464; P:protein modification; IEA. GO; GO:0006464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. Pfam; PF03133; TTL; 1. NON TER SEQUENCE 747 AA; 83854 MW; F90948EIS9BBES89 CRC64; Auery Match 96.0%; Score 2741; DB 2; Length 747; Best Local Similarity 94.0%; Pred. No. 1.1e-181; MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60	Homo sapiens (Human). Bulkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo MCBL TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V.; Cobley V.; Colostas; F: tubulin-tyrosine ligase activity; IEA. GO; GO:0006481; P: tubulin-tyrosine ligase activity; IEA. GO; GO:0006481; P: tubulin-tyrosine ligase activity; IEA. GO; GO:0006481; P: tubulin-tyrosine ligase. InterPro; IPR04344; Tub_tyr_lygase. InterPro; IPR04344; Tub_tyr_lygase. Pefam; PF03133; TTL; 1. NON TER. SEQUENCE 747 AA; B3854 MW; F90948E159BBE589 CRC64; Best Local Similarity 94.0%; Pred. No. 1.1e-181; MASSILKWVVSHOSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKIRGLPGQLVDIAC 24 [1]	Homo sapiens (Human). Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606; [1] NUCLEOTIDE SEQUENCE. Cobley V; (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL02237; CA14268c.1; -; Genomic_DNA. GO; GO:00046837; F:tubulin-tyrosine ligase activity; IEA. GO; GO:000464; P:protein modification; IEA. InterPro; IPR004344; Tub_tyr_lygase. Pfam; PF03133; TTL; 1. NON TER SEQÜENCE 747 AA; 83854 MW; F90948E159BE589 CRC64; GOesty Match 96.0%; Score 2741; DB 2; Length 747; Best Local Similarity 94.0%; Pred. No. 1.1e-181; MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGGLVDIAC 60 [Homo sapiens (Human). Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eutheri	Homo sapiens (Human). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Butheri	Homo sapiens (Human) Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; MCBI_TaxID=9606; NUCLEOTIDE SEQUENCE. CObley V.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0004835; F:tubulin-tyrosine ligase. InterPro; IPR004344; Tub_tyr_lygase. GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Bukaryota (Human) Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Hominidae; Mucleoride Seguence NCBI TaxID=9606; NUCLEOTIDE SEQUENCE. CODIGY V; NUCLEOTIDE SEQUENCE. CODIGY V; MUCLEOTIDE SEQUENCE. CODIGY V; SUDMITTER (MAY-2005) to the EMBL/GenBank/DBJ databases. EMBL; AL02237; CA142666.1; -; Genomic DMA. GO; GO:0004835; F:tubulin-tyrosine ligāse activity; IEA. GO; GO:0004844; Tub_tyr_lygase. InterPro; IPRO04344; Tub_tyr_lygase. InterPro; IPRO04344; Tub_tyr_lygase. InterPro; IPRO04344; Tub_tyr_lygase. INTR: NON TER SEQÜENCE 747 AA; 83854 MW; F90948E159BBE589 CRC64; SEQÜENCE 747 AA; 83854 MW; F90948E159BBE589 CRC64; MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC C9 INTERPROPERATER SEGUENCE AA; Mismatches 6; Indels 24; Gaps MASSILKWVVSHQSCSRSSRSRPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC C9 INTRIBITER SEQUENCE AA; MISMATCHEN CONTRIBUTION CONTRIBU

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                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933401B17 product:hypothetical Tubulin-tyrosine ligase
containing protein, full insert sequence.
Name=1700019P01Rik;
STPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLWRQPVVEPPFSGSDLCVAGVSVRRAR
                     STPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRRAR
                                                                         ROVLPVCNLKASASLLDAQPLKARGPSAMPDPAQGPPSPALQRDLGLKEBKGLPLALLAP
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                LRGAAESGGAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPL
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NUCLEOTIDE SEQUENCE.
STRAIN-C57BL/6J; TISSUE=Testis;
The FANTOM CONSORTIUM,
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QBCON7;
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STRAIN=C57BL/GJ TISSUBE-Testis;
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Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Submitted (JUL-201) to the EMBL/GenBank/DbBJ databases.
EMBL; MGI: 1922902; 1700019901Rik.
GO: GO:0016874; F:1igase activity; IEA.
GO: GO:0004644; P:protein modification; IEA.
InterPro; IPR00375; GPCR_Rhodpsn.
RinterPro; IPR00375; GPCR_Rhodpsn.
RinterPro; IPR00375; GPCR_Rhodpsn.
RinterPro; IPR003133; TTL: 1.
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2003 (TrEMBLrel. 25, Last amocration update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930524K07 product:hypothetical Tubulin-tyrosine ligase containing protein, full insert sequence.
Mus musculus (Mouse).
            QDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDIIKVAV
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279255; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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STRAIN=C57BL/6J; TISSUE=Testis; The FANTOM Consortium,

NUCLEOTIDE SEQUENCE

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STRAIN-C57BL/6J; TISSUE=Testis;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hirancko K., Hiraoka T., Hirozane T., Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Akawai J., Kojima Y., Konno H., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Konno M., Kono M., Koya S., Katoh H., Kawai J., Mumazaki A., Murata M., Nakamura M., Nakamura K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H., Saitoh H., Satai C., Saltoh H., Sakai C., Saltoh H., Saltoh H., Sakai C., Shinagawa A., Shiraki T., Sogabe Y., Tangami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Tubaki K., Submitted (JUL-2001) to the EmBL/Genbank/DDBJ databases.
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                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAINE-20949374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CSTBL/60; TISSUE-Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibbata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Itoh M., Aizawa K., Nagaoka T., Tashiro H., Itoh M., Sumi N., Ishii K., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Isawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RISNIKAWA T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RISNIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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518 AA; 59319 MW; 540C045659FAC0D6 CRC64;
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MGI, MGI:1922902; 1700019P01Rik.
GO; GO:0016874; F:ligase activity; IEA.
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Pfam; PF03133; TTL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
NAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVA
                  QDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV
                                                                        416 DRKLDRNCDIGNFELLWRQPAVELPPFNGSDLCVEGISVKKAKKQMPPIASVGLSESLLD
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                     ----DRSCDIGNFELLWROPVVEPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                             01-WAR-2003 (TrEWBLrel. 23, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Mus musculue 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A633053H17 product:HOTTL PROTEIN homolog.
Name=4833441J34Rik;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE=21085660; PubMed=112.7851; DOI=10.1038/35055500;
                                                                                                                                                                                                    AOPLKARGPSAMPDPAOGPPSPALORDLGLKEEKG 450
                                                                                                                                                                                                                                                                                           704 AA.
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
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The FANTOM Consortium,
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NUCLEOTIDE SEQUENCE.
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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Rusi MGI: 2141418; 483344124Rik.

Rusi MGI: 2141418; 483344124Rik.

Rusi MGI: 200004835; Fitubulin-tyrosine ligase activity; IEA.
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ka T.,
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                                                                                                                                                                                                                                                          MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibbata K., Nagadoka K., Nagadoka K., Nagadoka K., Nagadoka K., Nagadoka K., Nagadoka M., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumura S., Hazama M., Nishine T., Kashiwagi K., Vanamoto R., Mateumuro H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rixib integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity 40.19
226; Conservative
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SEQUENCE 704 AA;
                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                         NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                        302 HVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV-- 359
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                                                                                                                                                                                                                                                      417
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                                                                                      61
                                                                                                                                                                                                                                                                                          242 VQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQD 301
                                                                                                                                                                                                                                                                                                                                                                    501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPLA----LLAPLRGAAESGGAAQPTRTKA----AGKVELPACPCRHVDSQ--AP-NTG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ASSILKWIVSHQSCSRSSRSRPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIACK
                                                                                                      122 NRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQ
                                                                                                                                                                                                                                        KYIETPLLICDTKFDIROWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNA
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                       62 VCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 -- DRSCDIGNFELLWRQPVVEPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               PLKARGPS-----KBEKG
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=PCR rescued clones;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                               67;
                                      DB 2; Length 744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                             Indels
              DF661753E4AFF0DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                   36.6%; Score 1043.5; DB 2; 40.5%; Pred. No. 1e-63; tive 85; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 VPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPP
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           84683 MW;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBNDN8_HUMAN PRELIMINARY;
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             744 AA;
                                                Best Local Similarity
Matches 234; Conserv
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 NON TER
SEQUENCE
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                                      Query Match
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Name=DKFZp686D076;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Cheneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLPAHNMWTSTRFQEYLQRQRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 LLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLKARGPSAMPD 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CHRRMGVR----PAVPLLTQRGSGEARHHFPSLHTRA----QLPS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                              34.4%; Score 981.5; DB 2; Length 434; 46.7%; Pred. No. 9.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                         NIH MGC Project;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL833339; CAD38794.1; -; mRNA.
EMBL; BC098298; AAH98299.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                               GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:proctein modification; IEA.
InterPro; IER04344; Tub_tyr_ligase.
Pfam; PF03133; TTL; I.
                                                                                                                                                                                                                                                                                                                                                                                                         11 protein.
434 AA; 49433 MW; 9E79E6CA08651CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIYKQPAVEVPQYVGIRLLVEGFTIKK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $5-0CT-2004 (TrEMBLrel. 28, Created 25-0CT-2004 (TrEMBLrel. 28, Last st. 25-0CT-2004 (TrEMBLrel. 28, Last at Hypothetical protein DKFZp6860076.
                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
TISSUE=PCR rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGAWA3 HUMAN PRELIMINARY;
QGAWA3;
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DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 133
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                                                                                                                                                                                      Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 957.5; DB 2; Length 352;

; Pred. No. 3.5e-58;

55; Mismatches 91; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The German cDNA consortium;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     EMBL: BX648175; CAH10554.1; -; mRNA.

GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.

GO; GO:0006464; P:protein modification; IEA.

InterPro; IRR04344; Tub_tyr_lygase.

Pfan; PP03133; TTL; 1.
                                                                                                                                                                                                                                                                                                                                                                                    40257 MW; 49FD8E9CAE1CB20D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTLL3 HUMAN STANDARD; PRT; 352 AA. 0974AF, Q9U199. 41, Created)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tubulin tyrosine ligase-like protein 3 (HOTTL)
Name=TTLL3; ORFNames=PRO0207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLWRQPVVEPPPFSGSDLCVAGV-SVRRAR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:::||| | : : | ||| LIYKQPVTTSPASTPGPSCLLPMYSDTRAR 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                33.5%;
54.2%;
                                                                                                                                                                       The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 54.2
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 352 AA; 4
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                                                                                                                               NUCLEOTIDE SEQUENCE
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                                                                                    NCBI_TaxID=9606;
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Hypothetical
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                                                      This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                       254 PLLPAHNWWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY 313
                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNFE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
            deduced
                                                                                                                                                                                                                                                                                                                                                 74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                           KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                      134 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILBLAAADHPLSRDNKWVVQKYIETPLLICDT
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            new genes
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MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                         33.5%; Score 956.5; DB 1; Length 352; 54.2%; Pred. No. 4.1e-58;
                                                                                                                                                                                                                                                                              91; Indels
                            Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         M -> R (in dbSNP:2290305).
                                                                                                                                                                                                                                 49FD8E8118C7C20D CRC64;
            of 50
Liu M., He F.; "Functional prediction of the coding sequences of by analysis of CDNA clones from human fetal liver."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                  /FTId=VAR 020207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLWROPVVEPPPFSGSDLCVAGV-SVRRAR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 LIYKQPVTTSPASTPRPSCLLPMYSDTRAR 331
                                                                                                                                                                                                                                                                              55; Mismatches
                                                                                                                EMBL; AL096725; CAB46375.1; -; mRNA.
EMBL; AF078842; AAF23353.1; -; mRNA.
PIR; T12515; T12515.
Ensembl; ENSG0000156983; Homo sapiens.
                                                                                                                                                        HGNC; HGNC:24483; TTLL3.
InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
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                                                                                                                                                                                                                                                                   Best Local Similarity 54.2
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4KMS8 HUMAN PRELIMINARY;
Q4KMS8;
                                                                                                                                                                                               293
                                                                                                                                                                                                                             67
                                                                                                                                                                                      Ligase; Polymorphism.
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                                                                                                                                                                                                                                     352 AA;
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                                                                                                                                                                                                         290
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Romascein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
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Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 GADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRRLDRNCDTGAFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC098361; AAH98361.1; -; mRNA.
EMBL; BC099735; AAH99735.1; -; mRNA.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 11 SCAF14979, whole genome shotgun sequence.
ORFNames=GSTENG00027209001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al protein.
352 AA; 40381 MW; 49EF0C1118C7DD12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rescued clones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 54.2%
Matches 179; Conservative
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Q4RY08;
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NIH MGC Project;
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F2 BOVIN
Q58CT2_BOVIN PRELIMINARY;
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4833441J24Rik proteir
Name=4833441J24Rik;
Mus musculus (Mouse)
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                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FVB/N;
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                                                                                                            NUCLEOTIDE
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                                                                                                      Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattelli V., Katinka M., Vacherie B.,
Rotaud C., Lardier S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
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Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 TSLLQHVVEGSSHRRA-----DAKEE----QLHLPEDL--SKHKLPFVNAGVIATALRV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKYLKNDVGRSPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 ÖKHFEPARNRHPAVPGDNMWSCSQFRAFLHQÖGRSAEWDVVTVPGMOKAIIRALQTAQEQ 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIACKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetraodontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                              Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
.; CAAE01014979; CAG06724.1; -; Genomic_DNA.
JENCE 534 AA; 60130 MW; 62B5BBBB696B662B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.0%; Score 941.5; DB 2; 49.2%; Pred. No. 7.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.9e-57;
9; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 CD----IGNFELLWRQPVVEP--PPFSGSD 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodon nigroviridis (Green puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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Q922T0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 49.2 tes 192; Conservative
                                                                                                                                                                                                                                                                                                       Nature 431:946-957(2004)
                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                    NCBI_TaxID=99883;
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01-DEC-2001
01-OCT-2003
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RY STRAINE-PUB/N; TISSUE-Mammary tumor. C3;

RY RELINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIALINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchehot L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McBwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Raha P.J., McBwan P.J., Rodergren E.J., Lu X., Gibbs R.A.,

Raha P.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Mennerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 YGADFVFGEDFQPWLIEINASPTWAPSTAVTARLCAGVQADTLRVVIDRRLDRSCDTGAF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC006830, AAH06830.1; -; mRNA. Ensembl; ENSMUSG00000030276; Mus musculus. MGI: 2141418; 434102481k. GO; GO:0004835; R:tubulin-tyrosine ligase activity; IEA. GO; GO:000464; P:protein modification; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03133; TTL; 1.
SEQUENCE 266 AA; 30506 MW; P8E8FB52FA8B8E98 CRC64;
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60.6%; Pred. No. 9.1e-50;
iive 44; Mismatches 49;
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us-10-635-977-2.rup

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Q9VM91;
01-MAY-2000 (TrEMBLrel. 13,
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01-OCT-2003 (TERMBLE). 25,
CG11323-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 39.8%
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03133; TTL; 1.
                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                              NUCLEOTIDE SEQUENCE
    NCBI_TaxID=180454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GTKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 RHPLLPPDNMWSSQKFQAHLQETGAPNAWSTVIVPGMKAAVIHALQTSQDTVQCRKASFB 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD----- 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      TISSUE=Pooled,
MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
Gasas E., Waragese W.W., Cho J., Fahrenkrug S.C., Bennett G.L.,
Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
Keele J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harhay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.D.,
Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle."; Genome Res. 11:626-630(2001).
                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.3%; Score 807.5; DB 2; Length 261; 58.5%; Pred. No. 6.2e-48; ive 37; Mismatches 59; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AA; 29911 MW; 5F069784CA162017 CRC64;
                           LO-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Tubulin tyrosine ligase-like family, member 3.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 AA
                         Created)
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                                                                                                                                                                                                   Pecora; Bovidae; Bovinae; Bos.
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ORFNames=ENSANGG0000019848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BT021865; AAX46712.1;
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                    t0-MAY-2005 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 LSSSTSSLPWRCP
                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Pooled
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SEQUENCE
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288 EAKSVLEQIKSHWPQYALDGYLNIWIVKPGNKCRGRGIHLMNNIKQI--1AMVNPPIVSK 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 QCQALLARITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIACKVCQ 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 MKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              465 LLACQDNMDRRPNTFELYGADFMITEDFYPWLIEINSSPDLAPSTSVTARLCPQCVEDTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                             The Anopheles gambiae Sequence Committee;
Submitted (ARF-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Sphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                        preliminary data.

EMBL, AAAB01008980; EAA13905.2; -; Genomic DNA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006484; P:protein modification; IEA.
InterPro; IPR004344; Tub_tyr_lygase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 AA; 67109 MW; 8938D9EDD5935071 CRC64;
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Last annotation update)
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Adams W.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R. Adams W.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R. Adams W.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R. Sucton G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
R. Bandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfelifer B.D.,
R. Ballew R.M. Bauv A.M. Barendal J., Bayrakaraglu L., Beasley E.M.,
R. Beeson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
R. Burtis R.C., Chams D.A., Buller H., Cadicu E., Center A., Chandra I.,
R. Burtis R.C., Eusam D.A., Buller H., Cadicu E., Center A., Chandra I.,
R. Burtis R.D., Caller A., Denger S., Mankov B.C., Dunn P.,
R. Burtis R.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischman W.,
R.A. Goden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Borton K.J. Evangelista C.C., Ferraz C., Ferriera S., Pleischman W.,
R.A. Godek A., Gody F., Gorrell J.H., Gu Z., Gulbart W.M., Glasser K.,
R.A. Godok A., Gody F., Gorrell J.H., Gu Z., Gulbart W.M., Glasser K.,
A drink M., Kalush F., Rapen G.H., Ke Z., Kennison J.A., Kechnison D.A.,
R. Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Allen B.M., Moy M., Wurphy B., Murphy L., Murny D.M., Nelson D.L.,
R.M. Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
R. Shener K., Remington K., Stupkin M., Stupkin M.,
R. Spier E., Spiradling A.C., Stapleton M., Stupkin M., Shubskin M.,
R. Wassaman D.A., Wassamos I., Singson M., Stupkin M., Wassen D.J.,
R. Wassaman D.A., Wassern D.S., Wang S., Yau D.,
R. Wassaman D.A., Wassern D.S., Wang S., Yau D.,
R. Wassaman D.A., Wassern D.S., Wang S., Yau D.,
R. Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. Walliams S.M., Woodage T., Worley K., Zhu S., Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Biol. 3: RESEARCH0084.1-RESEARCH0084.20(2002)
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MEDLINE=22426070; PubMed=12537573;
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[2]
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systematic review."; Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 IPYSAIDFAYKRLVEYIDSCQHNDID-----FEDPPKIWEHDWDAFLFQHQQLVNEDGRI 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 SNS----RNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 QHDGGQRLEPMVKSCLSLVDKMKVHWPQYSLDGYQNNWIVKPANKCRGRGIILMDNLKKI 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 LELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LGVVNLSIASKSRYVVQKYIERPLILFQTKFDIRQWFLITNTQPLVVWFYRESYLRFS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 VIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPV 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                    51 LPGQLVDIACKVCQAYLGQLEHEDIDTSADAVED---LTEAEWEDLTQQYYSLVHGDAFI
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                                               Frise E., George R.,
Svirskas R., Smith E.,
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ORFNames-ENSANGGO000019845;
Anopheles gambiae str. PET.
Blkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                             / Match 25.3%; Score 722.5; DB 2; Length 992; Local Similarity 33.3%; Pred. No. 3e-41; National 175; Conservative 86; Mismatches 198; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H-----VDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLRGLK 526
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EMBL, AE003614, AAF52432.1; -; Genomic_DNA.
                                                                 Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas F Yu C., Rubin G.,
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            FlyBase; FBgn0031854; CG11323.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA
GO; GO:0006464; P:protein modification; IEA.
                                                                                                                                                                                                                                                                                                                                112255 MW; OFC34674C15BDAAD CRC64;
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01.MAR-2004 (TrEMBLrel. 26, Last sequence update)
01.MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                 В.
                                                                                                                                                                                                                            Ensembl; CG11323; Drosophila melanogaster.
                             Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer
Hoskins R., Stapleton M., Pacleb J., Park
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Q7PMD3;
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                NUCLEOTIDE SEQUENCE.
                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 RNY----FSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILEL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 AAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVT-DWNPLTIWFYKESYLRFSTQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 VDS----NPDVKYVAQKYIERPLLIHCTKFDIRQYFLITYTNNVLKVMMYRNCYLRFSSR 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 RFSLDKLDSAIHLCNNAVQK-YLKNDVGRSPLLPAHNMWTSTRFQEYLQRGRGAVWGSV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 IYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVT 343
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                      The Anopheles gambiae Sequence Committee,
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.5%; Score 584.5; DB 2; Length 501; Best Local Similarity 40.8%; Pred. No. 4.6e-32; Matches 135; Conservative 54; Mismatches 123; Indels 19
                                                                               STRAIN=PEST,
The Anopheles gambiae Sequence Committee,
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            EMBL/General Colliniary data.

Preliminary data.

EMBL; AAABOLO0890; EAA13971.3; -; Genomic DNA.

GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.

GO; GO:0006464; P:protein modification; IEA.

InterPro; IPR011761; ATP GRASP.

InterPro; IPR03133; TLL; 1.

PROSITE; PS50975; ATP GRASP; 1.
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501 AA; 58862 MW; 806539A2FD8E76DF CRC64;
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Search completed: April 4, 2006, 12:45:56 Job time: 82.9545 secs

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GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2006, 12:45:31; Search time 20.1115 Seconds (without alignments)
2588.231 Million cell updates/sec
Title: US-10-635-977-2
Perfect score: 2854
Sequence: 1 MASSILKWVVSHQSCSRSSR.....LRGLKTAREGALRPPPGGKGS 541
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

w	Description	hypothetical prote	- u	protein ZK1128.6 [hypothetical prote		protein C55A6.2 [i	hypothetical prote	tubulin-tyrosine 1	hypothetical prote	hypothetical prote		gp330 protein prec	probable reductase	tegument protein 6	probable transcrip	Ras guanine nucleo	hypothetical prote	synaptojanin, 170K	progesterone recep	transforming prote	suppressor of yeas		dominant autoantig	probable US snRNP-	FB19 protein - hum	hypothetical prote	BPLF1 protein - hu	hypothetical prote	transforming prote
SUMMARIES	ID	T12515	A45443	E88575	T27699	T20262	C89217	T20343	T37571	A96805	S48261	E83594	T42737	A70507	855659	T41104	S25716	T46394	S68448	A25923	A43817	151657	T31425	S53457	T39188	JE0291	G84897	QQBE8	T46910	B43817
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RESULT 2
A45443
Lubulin-tyrosine ligase (EC 6.3.2.25) [validated] - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Decies: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

filensin - bovine hypothetical prote	nook-containing pr cyclic beta 1-2 gl protein H28G03.2 [ALR protein - huma ALR protein - huma hypothetical prote	period protein hom microtubule-associ hypothetical prote	hypothetical prote homeotic protein A	stable tubule only hypothetical prote hypothetical prote
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Downy-2001 #text_change 09-Jul-2004
C;Accession: E88575
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A7500; MUID:9969613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: E88575
A;Steaus: preliminary
A;Molecule type: DNA
A;Residues: 1-640 cSTO>
A;Cross-references: UNIPROT:Q09647; UNIPARC:UPI000017A077; GB:chr_III; PIDN:CAA87425.1;
C;Genetics:
A;Amp position: 3
C;Accession: A45443
R;Ersfeld, K.; Wehland, J.; Plessmann, U.; Dodemont, H.; Gerke, V.; Weber, K.
J. Cell Biol. 120, 725-732, 1993
J. Cell Biol. 120, 725-732, 1993
A;Title: Characterization of the tubulin-tyrosine ligase.
A;Reference number: A45443; MUID:93147125; PMID:8093886
A;Reference number: A45443
A;Reference type: mRNA; protein
A;Residues: 1-379
A;Residues: 1-379
A;Residues: 1-379
A;Residues: 1-379
A;Residues: Leferences: UNIPROT:P38160; UNIPARC:UPI00001377A9; GB:X68453; GB:S54050; NID:g21
A;Reprimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:123858, NCBIP:123859)
C;Keywords: ligase
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56; Mismatches 118;
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Pred. No. 1.2e-11;
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25.6%; Pred. No. 7.66
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27699
R;Berks, M.
R;Berks, M.
R;Berke, M.
A;Reference number: Z20407
A;Accession: T27699
A;Accession: T27699
A;Accession: T27699
A;Accession: T27699
A;Accession: T27699
A;Kesidues: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 QDH----VEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTI
                                                                                                                                                                    DIKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDK---LDSAIHLCNNAVQKYLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:ZK1128.6
A;Map position: 3
A;Introns: 114/1; 208/3; 242/3; 334/3; 362/2; 405/2; 424/2; 550/2; 633/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
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: | |:: |:|| |:|| | ETDASRHV-IVKPPASARGTGISVTRKPKDFPTTATL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: 009647; A; Experimental source: clone ZK1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900
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585 DQLGVIDNRIFKRLTP
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Appendencial procesh Us. 13.9.9 "Caenorhabolitis elegans c) Accession: T20343; T22085
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A; Reference number: 219259
A; Residues: 1-662 < WIL>
A; Residues: 1-662 < WIL>
A; Experimental source: clone D2013
A; Experimental source: clone D2013
B; Matthews, P.
S; Matthews, P.
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tubulin-tyrosine ligase related protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: 03-Dec.1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37571
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
252 RSPLLPAHNWWTSTRFOEYLOROGRGAVWGSVIYPSMKKAIAHAMKVAQDHV--EPRKN- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 SADAVEDLTEAEWEDLTQQYYSL-VHGDAFISNSRNYFSQCQALLNRITSVNPQTDIDGL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 RNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLI----- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 HNVWIVKPWNLARGMDMTVTEDLNQIIRMI-----ETGPKIVCEYIPRPLLFPRPDNG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 CDTKFDIROWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKL-DSAIHLCNNAVQKYLKND 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 VGRSPLLPAHNMWISTRFQEYLQRQGRGAVWGSV---IYPSMKKAI-AHAMKVAQDHVEP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488 NKVKFDLRYIVFLNGIAPVTAYVYNRFWIRFAINEFSLSNFEDVETHF---TVFNYL--D 542
                                                                 830 SSEDL--GHKWTLGALLRYVENEGKDA---KLLMLRIEDLIVKSLLSIQNSVATASRTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 NVQSRAMYGVDIMLQHGDNDVIKSTLLEINFMPD-----TTRACQYYPDFADTV 645
                                                                                                                                                                          306 RKNSFELYGADFVLGRD----FRPWLIEINSSPTMHPSTPVTAQLCAQVQE--DTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
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                                                                                                                                                                                                                                                                                                                                                                                 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 78/2; 114/3; 330/3; 471/1; 521/2; 587/2
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein D2013.9
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A;Map position: 2
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: To-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89217
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:017720; UNIPARC:UPI000017A066; EMBL:281051; PIDN:CAB02862.2; A;Experimental source: clone C55A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:C55Ab.z
A;Map position: 5
A;Introns: 32/3; 68/1; 107/3; 201/3; 273/1; 364/3; 407/3; 460/3; 476/2; 534/2; 677/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 WFLVTDWNPLTIWPYKESYLRFSTQRF--SLDKLDS--AIHLCNNAVQK----YLKNDVG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHV--EPRKN- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               825 SSEDL--GHKWTLGALLRYVENEGKDA---KLLMLRIEDLIVKSLLSIQNSVATASRTNL 879
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                  hypothetical protein C55A6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T20262 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T20262 R;Kershaw, J. Submitted to the EMBL Data Library, October 1996 A;Reference number: Z19243 A;Reference number: Z19262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 209.5; DB 2; Length 1198; 25.5%; Pred. No. 3.1e-07; ive 57; Mismatches 87; Indels 31;
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                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1198 <WIL>
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Best Local Similarity
Matches 60; Conserva
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Best Local Similarity
Matches 60; Conserv
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140 WIIKPAAKSRGRDIVCMDRVEEI--
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                                                                                             PLLPAHNMWISTRFQEYLORG-
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A;Map position: 2R
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizoney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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A;Accession: T37571
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule: 1-403 cBAD>
A;Cross-references: UNIPROT:Q10438; UNIPARC:UP1000013A94B; EMBL:Z70721; PIDN:CAA94694.1;
A;Experimental source: strain 972h-; cosmid c12B10
C;Genetics:
A;Gene:SPAC12B10.04
A;Map position: 1
A;Introns: 320/3; 348/3
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                                                                                                                                                                                                                                                                                           ---EDLTEAEWEDLTQQYYSLVHGDAFISNS----
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                                                                                                                                                                                                                                                                                                                                                                    ---RNYFSQCQALLNRITSVNPQTDIDGLRNI----WIIKPAAKSRGRDIVCMDRVEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                              163 LEL-------AAADHPLSRDNK------WVVQKYIETPLLICDTKFDI
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25.3%; Pred. No. 0.0022;
ive 36; Mismatches 93;
                                                                                                                                                                                                                                 Pred. No. 0.00027;
65; Mismatches 127;
                                                                                                                                                                                                                 5.6%; Score 161; DB 2; 20.6%; Pred. No. 0.00027;
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Matches 72; Conserv
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Best Local Simi
Matches 55;
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A;Molecule type: DNA
A;Residues: 167-351, TPE',356-449,'A',451-562,'R',564-753 <DEK>
A;Cross-references: UNIPARC:UPI0000168D37; EMBL:X69881; NID:94086; PIDN:CAA49508.1; PID
C;Genetics:
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A/Accession: DA/Accession: D
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KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS 253
                                                                                                                                                                                                                                       RGAVWGSV----IYPSMK---KAIAHAMK 297
                                                                                                                                                                                                                                                                                                                                               749 ----LNHKPTAEFVREFEQEHNDFYAFHFVNNTIQLSIVKWMDIHEKVKOVIRAVFEAAA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YBR094w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YBR0821
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence revision 11-Aug-1995 #text_change 09-Jul-2004
C;Date: 01-Aug-1995 #sequence revision 11-Aug-1995 #text_change 09-Jul-2004
C;Date: 01-Aug-1995 #sequence revision 11-Yeast 10, 1353-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: S48255; MUID:95208357; PMID:7900426
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                                                                               172 LSRDNKWVVQKYIETPLLIC---DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRF--
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C; Accession: T42737
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of A;Reference number: A58173; MUID:95024033; PMID:7937880
A;Accession: T4273
A;Accession: T4273
A;Accession: T4273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Holecule type: mANA
A;Residues: 1-4660 cSAI>
A;Cross-references: UNIPROT:P98158; UNIPARC:UP1000013C4B4; EMBL:L34049; NID:9561852; P
A;Experimental source: strain Sprague-Dawley; kidney
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-bindi
F;1-25/Domain: signal sequence #status predicted cSIG>
F;26-4660/Product: gp330 protein #status predicted cMAT>
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                     C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
N; Alternate names: megalin
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K.; Lim,
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A.Racesalon: B83594
A.Status: preliminary
A.Ratus: preliminary
A.Residues: 1-2472 <STO>
A.Residues: 1-2472 <STO>
A.Residues: 1-2472 <STO>
A.Residues: 1-2472 <STO>
A.Residues: 1-2472 <STO>
A.Residues: 1-2472 <STO>
A.Gross-references: UNIPROT:091696; UNIPARC:UPI00000C5045; GB:AE004478; GB:AE004091; NID A.Gene: PA0413
                               still frameshift probable component of chemotactic signal transduction system PA04131 C.Species: Pseudomonas aeruginosa C.Species: Pseudomonas aeruginosa C.Baces: D.Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C.Bacession: E83594 R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yaun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. in Lory, S.; Jolson, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 QEYLOROGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWL 327
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DHETVDAERARLAGPDRDAMRSVVGALCEELVRIKDSL---DLFVRSDRGHPSELDALLA
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4.6%; Score 130; DB 2; Length 2472;
Best Local Similarity 19.7%; Pred. No. 0.79;
Matches 122; Conservative 81; Mismatches 203; Indels 21.
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| PVQPINPPAQNVPVSLLPPP 857
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gp330 protein precursor -
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                                                                                                       66 YLGQLEH-EDIDTSADAVEDLTEAEWEDLTQQYYS-LVHGDAFISNSRNYFSQCQALLNR
                                                                                                                                  124 ITSVNPQTDID-GLRNIWIIKP---AAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWV
                                                                                                                                                                                                                                         331 N-----SSPTWHPSTPVTAQL-----CAQVQEDTIKVAVDRSCDIGNFELLWRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4430 LTFVIVIIVGALVLVGLFHYRKTGSLLPTLP-KLPSLSSLAKPSENGNGVTFRSGADVNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 -----PPSPALQRDLGLKE----EKG-LPLALLAPLRGAAESGGAAQPTRTKAAGKVE
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                                                                                                                                                                                                                                                                                                            180 VQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCN
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Query Match
4.3%; Score 124; DB 2; Length 4660;
Best Local Similarity 19.7%; Pred. No. 5.6;
Matches 118; Conservative 69; Mismatches 191; Indels 222;
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probable transcription factor subunit, TPR domains - fission yeast (Schizosaccharomyce C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: T41104
R; Purnelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A; Reference number: Z21964
A; Refatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1006 < PUR>A; Residues: 1-1006 < PUR>A; Residues: 1-1006 < PUR>A; Cosmid c16C4
B; Experimental source: strain 972h-; cosmid c16C4
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                                                                                                                                                                                                                                                                     151 BAQKLAEBIVRI-------DNNVIAAWKMLGECHRORGKVNIEKCLIAWMA 196
2185 EAVEAKMSQIEQAIEGADVYEAVAGTPLEAPVARALRLIRAARDEAAGLKGQIDEGERAY 2244
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                                                                                                                                                                                                                                                                                                                                                                         374 QPVVEPPPFSGSDLCVAGVSVRRARRQVLPVC--NLKASASLLDAQPLKARGPSAMPDPA 431
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                                                                                                                                      2245 VQGVERAGEGGEPPAKPKAEIPKKLLTYEQTLSLANLPEDFQKNVLQNETLMLNQLREYL
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                                                                                                                                                                                                                              330 ----INSSPTWHPST--PVTAQLCAQVQEDTIKVAV-----DRSCDIGNFELLWR-
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21.0%; Pred. No. 2.6;
tive 58; Mismatches 137; Indels
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Best Local Similarity 21.0%
Matches 92; Conservative
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70507
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-882 < COL>
A;Cross-references: UNIPROT:033268; UNIPARC:UP10000004F63; GB:297991; GB:AL123456; NID:9
A;Experimental source: strain H37Rv
C;Genetics
A;Genetics
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tegument protein 64 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Caccession: S55659
C,Caccession: S55659
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55659
A;Accession: S55659
A;Accession: Lype: DNA
A;Molecule type: DNA
A;Residues: 1-3436 <TEL>
A;Accession: S5666; UNIPARC:UPI0000067BF4; GB:UZ0824; NID:g695172; PIDN:A;Coss-references: UNIPROT:Q66666; UNIPARC:UPI0000067BF4; GB:UZ0824; NID:g695172; PIDN:A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Rebruary 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 AQPLKARGPSAMPD-----PAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAES 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 AKQAQERAPKAAPKAAAPVTPVEAPAEAPQAPA------PAAPAAPVKGLGMA 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.2%; Score 120; DB 2; Length 882; Best Local Similarity 27.2%; Pred. No. 0.98; Matches 43; Conservative 11; Mismatches 52; Indels
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Scoring table: BLOSUM62	BLOSUM62

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This invention relates to a novel testis-specific tubulin tyrosine-ligase

-like polypeptide, designated the BGS-42 polypeptide. The invention may

be useful for the development of compounds with a cytostatic, respiratory

Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

antinalammatory, anabolic, hypertensive, osteopathic, nootropic,

antingarkinsonian, antiathritic, antiasthmatic, anti-HIV, antibacterial,

immunosuppressive, antiasbornteic or dermatological activity acting as

tyrosine ligase modulators. In addition, the disclosed sequences may be

tyrosine ligase modulators. In addition, the disclosed sequences may be

cused for diagnosing a pathological condition or a susceptibility to a

cused for diagnosing a pathological condition as a disorder related to aberrant

cused for diagnosing a pathological condition, as disorder related to aberrant

cused for diagnosing a pathological condition, as disorder related to aberrant

cused for diagnosing a pathological condition, as disorder related to aberrant

cused for diagnosing a medical condition, as disorder related to aberrant

cubulin ligase activity, a disorder related to aberrant

cubulin ligase activity, a disorder related to aberrant

cubulin ligase activity, a disorder related to aberrant

cubulin ligase activity, a disorder related to aberrant

cubulin ligase activity, a disorder related to aberrant

cubulin ligase activity, a disorder, colon cancer, pubmonary disorders,

cubulin ligase activity, a disorders, colon cancer, sometri, concer,

cubulin ligase activity, a disorders, colon cancer, propeptide, polynucleotide, or their modulators are also useful for

cueval disorders, brain cancer, liver cancer, or proliferation, cof the testis, lung, small intestine, brain or lymph tissue. The BGS

creating infertility, Cushings syndrome, emphysema, preumonia, Addison's

disease, acromegaly, Alzheimer's disease, or Parkinson's disease.

creation including arthritis, asthma, AlbS, sepsis, acne, Sjogren's

chiesease or scleroderma. The antibodies ma 480 540 540 240 360 420 361 RSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLK 420 120 180 61 KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQAL 120 121 LNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVV 180 AVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ 300 241 AVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ 300 1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC 60 1 MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC LNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVV DHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVD RSCDIGNFELLWRQPVVEPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLK ELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPPGGKG ELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPGGKG QKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN **ARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKV** Gaps . 0 Query Match
100.0%; Score 2854; DB 8; Length 541;
Best Local Similarity 100.0%; Pred. No. 4.2e-264;
Matches 541; Conservative 0; Mismatches 0; Indels 0 Claim 5; SEQ ID NO 2; 343pp; English. Sequence 541 AA; 241 181 481 301 421 셤 qq 8 \times 9 g ò ď ò g δ ò ð ò 유 ò ઠ 셤

S 541

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This invention relates to a novel testis-specific tubulin tyrosine-ligase

"Inke polypeptide, designated the BGS-42 polypeptide. The invention may

"Like polypeptide, designated the BGS-42 polypeptide. The invention may

"Cen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,

"Cantinflammatory, anabolic, hypertensive, osteopathic, nootropic,

antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,

"Communosuppressive, antieborratheic or dematological activity acting as

tyrosine ligase modulators. In addition, the disclosed sequences may be

useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be

used for diagnosing a pathological condition or a susceptibility to a

pathological condition in a subject, and for preventing, treating or

ameliorating a medical condition, such as a disorder related to aberrant

tubulin ligase activity, a disorder related to aberrant tubulin
carboxypeptidas activity, adsorder related to aberrant tubulin
carboxypeptidas activity, adsorders, colon cancer, stomach cancer,

carboxypeptidas activity, adsorders, colon cancer, stomach cancer,

carboxypeptidas activity, adsorders, colon cancer, stomach cancer,

carboxypeptidas activity, adsorders, inver cancer, or proliferative condition

carboxypeptides, plang, small intestine, brain or lymph tissue. The BGS-42

polypeptide, polymucleotide, or their modulators are also useful for

treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's BGS-42 polypeptide; cytostaelity are interpolypeptide; cytostaelity respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive; osteopathic; noctropic; antiparkinsonian; antiatrhitic; antiasthmatic; anti-parkinsonian; antisthritic; antiasthmatic; anti-parkinsonian; antisteborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular disorder; pulmonary disorder; lung cancer; gastrointestinal disorder; concer; proliferative condition; restis; lung; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; phanin; lymph tissue; infertility; Cushing's syndrome; parkinson's disease; archifertility; Alzheimer's disease; parkinson's disease; arthritis; asthma; ADS; е. 9 New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular Human tubulin tyrosine ligase protein consensus sequence SeqID13. testis-specific tubulin tyrosine-ligase-like polypeptide; sepsis; acne; Sjogren's disease; scleroderma; human. Example 4; SEQ ID NO 13; 343pp; English. ADJ93365 standard; protein; 541 AA. 8 39-JUL-2003; 2003WO-US021605. 09-JUL-2002; 2002US-0394725P. (BRIM) BRISTOL-MYERS SQUIBB Nelson TC; (first entry) WPI; 2004-099381/10. Wu S, N-PSDB; ADJ93364. MO2004005487-A2. S 541 Homo sapiens 06-MAY-2004 15-JAN-2004. Synthetic. disorders. Feder JN, ADJ93365; ADJ93365

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testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
seteopathic; nootropic; antiparkinsonian; antischritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antischorrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
      The BGS
                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                      240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVQKYLKNDVGRSPLLPAHNMTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKV 480
disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-2 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Slogren's disease or scleroderma. The antibodies may be used to purify, detect and trarget the BGS-42 polypeptides. The present sequence is that of the tubulin tyrosine ligase protein consensus sequence which was used in the exemplification of the invention.
                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                         MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC
                                                                                                                                                                                                                                                         MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIAC
                                                                                                                                                                                                                                                                                                                                                                                                                    QKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 RSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLK
                                                                                                                                                                                                                                                                                                                                                      LNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSCDIGNFELLWRQPVVEPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELPACPCRHYDSQAPNTGVPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPGGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKV
                                                                                                                                                                                               Gaps
                                                                                                                                                                                              .;
0
                                                                                                                                                                Length 541;
                                                                                                                                                                                            2; Indels
                                                                                                                                                            Score 2843; DB 8;
Pred. No. 4.8e-263;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BGS-42 protein-related TTL1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ93366 standard; protein; 293 AA.
                                                                                                                                                           Ouery Match
Best Local Similarity 99.6%;
Matches 539; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                             Sequence 541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
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This invention relates to a novel testis-specific tubulin tyrosine-ligase—
like polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
CD be useful for the development of compounds with a cytostatic, respiratory
CG mitinflammatory, anabolic, hypertensive, osteopathic, nootropic,
antinflammatory, anabolic, hypertensive, osteopathic, nootropic,
antinflammatory anabolic, hypertensive, osteopathic, nootropic,
antinflammatory antiarthritic, antiasthmatic, anti-HIV, antibacterial,
communosuppressive, antiasthritic, antiasthmatic, anti-HIV, antibacterial,
communosuppressive, antiasthritic, antiasthmatic, anti-HIV, antibacterial,
compared for diagnosing a pathological condition, the disclosed sequences may be
compared for diagnosing a pathological condition, a susceptibility to a
compared for diagnosing a pathological condition, such as a disorder related to aberrant
compared and medical condition, such as a disorder related to aberrant
cubulin ligase activity, aberrant cellular proliferation, reproductive
carboxypeptidase activity, aberrant cellular proliferation, reproductive
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
companies, lung small incestine, brain or lymph tissue. The BGS-42
colypeptide, polymclectide, or their modulators are also useful for
ctreating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's
disorders including arthritis asthma, AIDS, sepsis, and, years
consequence is that of the TILI
condisorate the BGS-42 polypeptides apersent sequence is that of the TILI
condisoration of the human BGS-42 protein of the invention.
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gastrointestinal disorder; colon cancer; stomach cancer; neural disorder; brain cancer; liver cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; immunological disorder; arthritis; asthma; AIDS; sepsis; acne; Sjogren's disease; scleroderma; human; TTL1 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
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Pred. No. 2.2e-140;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 14; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                    09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                                                           09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                                                                                                                                                                                                                                             Nelson TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-099381/10.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Feder JN, Wu S,
                                                                                                                                                                                                     WO2004005487-A2.
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                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                 15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel testis-specific tubulin tyrosine-ligase—like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory-Gen, gastrointestinal-Gen, neuroprofective, endocrine-Gen, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiarthritic, antisthmatic, anti-HIV, antibacterial, immunosuppressive, antisebornheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to a berrant tubulin ligase activity, a desrant cellular proliferation, reproductive
                                                                                                                                                                                                                                                                                                   testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; neural disorder;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; arthritis; asthma; AlDS;
                                                         240
121 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular
                                           YGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 365
                                                                                                    sepsis; acne; Sjogren's disease; scleroderma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4; 343pp; English.
                                                                                                                                                                                                                                                                              Human BGS-42 protein sequence SegID4
                                                                                                                                                                                         Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                         ADJ93360 standard; protein; 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-2002; 2002US-0394725P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson TC;
                                                                                                                                                                                                                                                06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004005487-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders.
                                                                                                                                                                                                                     ADJ93360;
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                                                                                     313
                               253
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disorders, testicular disorders, testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neutral disorders, brain cancer, liver cancer, or proliferative candition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polynucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the human BGS-42 protein (partial sequence) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                133 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGNFELLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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T;
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0
                                                                                                                                                                                                                                                                                                                                                       Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Otsuki
                                                                                                                                                                                                                                                                                                                                                     Query Match 45.5%; Score 1299; DB 8; L
Best Local Similarity 100.0%; Pred. No. 1.7e-115;
Matches 242; Conservative 0; Mismatches 0;
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Wakamatsu A, Nagai K,
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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                                                                                                                                                                                                                                                                                                               Sequence 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RO 242
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Ishii S,
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Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

full-

Claim 8; SEQ ID NO 15921; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisentary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence, where the
complementary strand of a polynucleotide of sequence complementary to a
complementary strand of a polynucleotide of sequence where the
complementary strand of a polynucleotide of sequence where the
complementary strand of a polynucleotide of sequence where the
complementary strand of a polynucleotide of sequence where the
complementary strand of a polynucleotide of sequence where the
complementary strand of a polynucleotides and the combination of
the 5'-end sequence sets as least 15 nucleotides and the combination.
The primers are useful for synthesising polynucleotides,
complementary. The primers are useful for synthesising polynucleotides,
the full-length cDNAs. The primers are also useful for the
comparable and or diagnosis of the abnormality of the full-length
comparable and a polynucleotides and AAH13633 to AAH13628 represent
complementary strands and sequences; and a sequence of the
complementary strands and one used in the exemplification of the present invention

Sequence 744 AA;

12; 121 261 241 301 441 HVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV-- 359 501 122 NRITSVNPOTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQ 181 322 KYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNS 381 -- DRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDAQ 417 61 62 VCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALL ASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAENAEAKLRGLPGQLVDIACK KYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNA **VQKYLKNDVGRSPLLPAHNMTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQD** --KEEKG Gaps 129 DB 4; Length 744; 192; Indels PLKARGPS-----AMPDPAQGPPSPALQRDLGL----36.6%; Score 1043.5; DB 40.5%; Pred. No. 3.2e-90; ive 85; Mismatches 192 Matches 234; Conservative Query Match Best Local Similarity 182 242 302 442 360 502 418 셤 ઠે g ò 셤 ઠે ð a ઠે 쉽 8 셤 ò g ò

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Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder; cell proliferative disorder; inflammatory disorder; prion disease; vesicle trafficking disorder; gastrointestinal disorder; muscle disorder; neurological disorder; cell moltlity disorder; reproductive disorder; spinal cord disease; central nervous system disorder; mental disorder;
                                                                                                                                                                                                                                                                                                                            Kearney
                                                                                                                                                                                                                                                                                                                   Hillman JL;
Batra S, 1
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|:| |
---SPLKPLP 704
                                                                                                                                                                                                                                                                                                                   Baughn MR
Burford 1
                                                                                                   Human cytoskeleton-associated protein (CYSKP) #5.
                                                                                                                                                                                                                                                                                                                   J, Lu DAM,
, Bandman O,
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                                                AAU74334 standard; protein; 488
                                                                                                                                                                                                                                               05-MAY-2000; 2000US-0201960P.
08-MAY-2000; 2000US-0202739P.
05-UIN-2000; 2000US-0209705P.
07-JUN-2000; 2000US-0210970FP.
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                                                                                                                                                                                                                                                                                                                  Au-Young J,
Yao MG,
                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                                 (first entry)
                                                                                                                                                             gene therapy; cancer.
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N-PSDB; AAS99894.
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Y, Lal P,
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                                                                                                                                                                              sapiens.
                                                                                  12-MAR-2002
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                                                                 AAU74334;
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Azimzai N
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disorders.

New cytoskeleton-associated proteins and polynucleotides, useful fo diagnosing, preventing and treating cell proliferative, autoimmune, inflammatory, neurological, cell motility, reproductive and muscle

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Claim 1; Page 130-131; 194pp; English.

The invention relates to human cytoskeleton-associated polypeptides
(CYSKP) and their associated polynucleotide sequences. The sequences are useful in the treatment of disorders associated with overexpression or underexpression of CYSKP in a patient. The disorders include cell
underexpression of CYSKP in a patient. The disorders include cell
proliferative disorders (such as cancer, actinic keratosis,
arteriosclarosis, cirrhosis, hepatitis and psoriasis),
autoimmune/inflammatory disorders (such as, asthma, atherosclarosis,
cutoimmune/inflammatory disorders (such as, asthma, atherosclarosis,
osteoporosis, Crohn's disease, rheumatoria arthritis, diabetes mellitus
and anaemia), vesicle trafficking disorders (such as
hypertcholesterolaemia, diabetes insipidus, Grave's disease and goitre),
as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,
disorders (such as endometriosis and polycystic ovary syndrome), muscle
disorders (such as endometriosis and polycystic ovary syndrome), muscle
disorders (such as myocarditis, migraine, hypertension, hypoglycaemia,
myocardial infarction, epilepsy and muscular dystrophy, appinal cord
cerebral palsy and mental disorders (such as anxiety and schizophrenia).
Sequences AAU74330-AAU74363 represent human CYSKP of the invention

Sequence 488 AA;

LPLA----LLAPLRGAAESGGAAQPTRTKA----AGKVELPACPCRHVDSQ--AP-NTG 498 615 LPTAKVFISLPPNLDFKVAPSILKPRKAPALLCLRGPQLEVPCCLCPLKSEQFLAPVGRS 674

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499 VPVAQPAKSWDPNQLNAHPLEPVLRGLKTAEGALRPPP 536

556 PLLTQRGSGEARHHFPSLHTKAQ-LPSPHVLRHQGQVLRRQHSKLVGTKALSTTGKALRT

20-JUN-2001; 2001US-0300001P.

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                                                                                                                                                                                                                                                                                                                                                                                     MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; hemostatic; nephrotropic; antiameamic; antiporatiatic; hepatotropic; denotery; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crobn's disease; acquired immunodeficiency syndrome; AIDS; goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                             61
                                                                                                                      KFDIRQMFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                       GADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNFE
                                                                                                                                                                                                                                                                                                                                            DIDKDLEAPLYLTPEGWSLFLORYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDM
                                                                                                      DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                                                                                                             PLLPAHNMWTSTRFQEYLQRGGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                   DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                         Gaps
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                           20;
 Length 488;
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                           Indels
35.5%; Score 1013; DB 5;
45.5%; Pred. No. 1.4e-87;
iive 68; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                          LIYKOPAVEVPOYVGIRLLVEGFTIKK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MDDT polypeptide SEQ ID 459
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2001US-0280067P.
2001US-0280068P.
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2001US-0291829P.
2001US-0291849P.
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2001US-0299776P.
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                           Conservative
  Query Match
Best Local Similarity
Matches 214; Conserv
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17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
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29-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVM 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis, ABU11450-ABU11845 represent the MDDT polynucleotides encoded by ABU11450-ABU11845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                               New purified disease detection and treatment molecule proteins and polymucloctides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AIHLCHNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 EFVDEALCACEEYLSNLAHMDIDKOLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 HAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQED
                                                                                                           EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                Jones AL, Tran AB, Dahl CR, Gietzen D, Curum C, Jones AL, Tran AB, Dahl CR, Gietzen D, Curum CK, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR, SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin E H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIXVAV----DRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGV-SVRRAR 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Mismatches 101; Indels
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                                    (INCY-) INCYTE GENOMICS INC
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                                                                     Daffo A, Jones AL, Trar Dufour GE, Hilman JL, Daugherty SC, Dam TC, I Peralta CH, David MH, I Flores V, Marwaha R, Lk
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Best Local Similarity
                                                                                                                                                                                             WPI; 2003-058431/05.
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ID AAB5
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AAB58909 standard; protein; 362

DHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSL

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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB59711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention are isolation and characterisation of the DNA and protein sequences of the control of the breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunouppressive; noctropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabatic; antibarmatory; anticulex; vulnerary; uniconvulsant; antibacterial; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly continued and agonists may also be used in the diagnosis of cancer, proteins, agonists and adomists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's cardiovascular disorders such as mycoardial ischaemias, wound healing; and allergies and ulcerative colitis; and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional and envisional
                                                                                                                  Breast and ovarian cancer associated antigen protein sequence SEQ ID 617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                  Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroidiits; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 1056-1057; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US005881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-611515/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF21812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200055173-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                         27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000.
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   AABS8909;
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9 RGVPYQ------LGPHGHRQ---GLEAPLYLTPEGWSLFLQRYYQVVHEGAELR 109 NSRNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEBILELAAA

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92; Indels 19; Gaps Length 362;

34.0%; Score 969.5; DB 3; 52.0%; Pred. No. 1.3e-83; iive 58; Mismatches 92;

Matches 183; Conservative

Similarity

Query Match Best Local S

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348
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                                                    288
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                                                                                                                                                             234 KDAVIHALQTSQDTVQCRKASFELYGADFVFGEDFQPWLIEINASPTWAPSTAVTARLCA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotroppic, vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianaetic; antidiabetic; antianaemic; antibacterial; antifungal; antitheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; scholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; brone damage; cartilage damage; antiinflammatory disease; coagulation;
DKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSM
                                                                    KKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frame X,
                                                                                                                                                                                                349 QVQEDTIKVAV----DRSCDIGNFELLWRQPVVEPPPFSGSDLCVAGVSVRR 396
                                                                                                                                                                                                                     294 GVQADTLRVVIDRXLDRNCDTGAFELIYKQPAVEVPQYVGIRLLVEGFTIKK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF2769 polypeptide sequence SEQ ID NO:5538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 4720-4721; 5507pp; English.
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                                                                                                                                                                                                                                                                                                                              AAB43005 standard, protein, 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO-US008621.
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99US-0127728P.
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; contraceptive.
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05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 HLDTQVQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNG 113
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369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological, immunosuppressive; antinflammatory; antibacterial, antiviral; antifungal; antirheumatic; antihyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, disorders, osteoarthritis, graft vs host disease, cardiovascular disease, storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, nootropic, immunosuppressant, cytostatic, gene therapy, cancer, peripheral nervous system; CMS, Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic, amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic, chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                             74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLLPAHNMWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLLPPDNWWSSQRFQAHLQEMGAPNAWSTIIVPGMKDAVIHALQTSQDTVQCRKASFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNFE
                                                                                                                                                                                                                                                                      coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                33.5%; Score 956.5; DB 3; Length 352; 54.2%; Pred. No. 2.2e-82; ive 55; Mismatches 91; Indels 5.
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLWRQPVVEPPFSGSDLCVAGV-SVRRAR 398
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 179; Conserv
                                                                                                                                                                                                                                                                                                                Sequence 352 AA;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymocleotides are useful in gene therapy. A composition containing a polypeptide or polymocleotide of the invention may be used to traat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinhetic activity, chemotactic/chemokinhetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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Zhao QA;
                                                                                                                                                                                                                                                                                   nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 DGLRNIWIIKPAAKSRGRDIVCMDRVEBILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFDIRQWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVQKYLKNDVGRS
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                                                                                                                                                                         Ren F, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.5%; Score 956.5; DB 4; Length 352;
54.2%; Pred. No. 2.2e-82;
iive 55; Mismatches 91; Indels 5.
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Yang Y,
                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                        Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 2595; 10078pp;
                                                                                                                                                                                                                                                                                                     central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ93457 standard; protein; 352
21-JAN-2000; 2000US-00488725.
25-AFR-2000; 2000US-0059317.
20-UUN-2000; 2000US-00598042.
19-UUL-2000; 2000US-00633150.
14-SEP-2000; 2000US-00653450.
19-CTT-2000; 2000US-0063312.
29-NOV-2000; 2000US-0073344.
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Best Local Similarity
                                                                                                                                                                                                                                       WPI; 2001-442253/47.
                                                                                                                                              HYSE-\ HYSEO INC
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                                                                                                                                                                                          Wang J,
Zhou P,
                                                                                                                                                                                                                                                                                    Novel
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Gaps

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91; DB 8;

Pred. No. 2.2e-82;

33.5%; Scor. 54.2%; Pred. No. 2.2. ...e. 55; Mismatches

Length 352; Indels 193 121 253 313

PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY

194

GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNFE

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(first entry)

74 DIDTSADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 133

2 DIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDM 134 DGLRNIWIIKPAAKSRGRDIVCMDRVEBILELAAADHPLSRDNKWVVQKYIETPLLICDT 62 EGDRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVWKDGKWVVQKYIERPLLIFGT KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS

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122 KFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNSVHLCNNSIQKHLENSCHRH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 LLWRQPVVEPPFSGSDLCVAGV-SVRRAR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 LIYKOPVTTSPASTPRPSCLLPMYSDTRAR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM80420 standard; protein; 352
                                                                             Best Local Similarity 54.2
Matches 179; Conservative
Sequence 352 AA;
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                                                   Query Match
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                                                                                                                                                testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostazic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antinflammatory; anabolic; hypertensive;
osteopathic; noctropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modilator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease, acromegaly; Altshämer's disease;
sepsis; acne; Sjogren's disease; scleroderma; human; HOTTL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 7; 343pp; English.
                                                                                                     protein sequence SeqID2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feder JN, Wu S, Nelson TC;
                                              (first entry)
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                                                                                                     Human HOTTL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                           06-MAY-2004
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Tumour-associated antigenic target (TAT) polypeptide PRO80956, SEQ:1058.
                                                                                                                                                                                                                                Tumour-associated antigenic target; TAT; human; overexpression; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                     tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; badder cancer; pancreatic cancer; cerrical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; SEQ ID NO 1058; 7273pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-347921/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu TD,
This invention relates to a novel testis-specific tubulin tyrosine-ligase like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory cen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiinflammatory, antisebritaic, antiasthmatic, antiinflamtory acting as tyrosine ligase modulators. In addition, the disclosed sequences may be tyrosine ligase modulators. In addition, the disclosed sequences may be tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be used for diagnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, pulmonary disorders, lung small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymelectide, or their modulators are also useful for reating infertility. Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological cisorapers including arthritis, asthma, AlDS, sepsie, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of the human CT arget the BGS-42 polypeptide to the invention. Note: The present sequence obtained from company.
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22-MAR-2002; 2002JP-00137785.

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide so equencies at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosing of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cervical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, colorectal cancer, cervical cancer, cancers of the central used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence cancer says and percents a TAT polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 DIDTSADAVEDLIEAEWEDLIQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLLPPDNWWSSQRFQAHLQEMGAPNAWSTIIVPGMKDAVIHALQTSQDTVQCRKASFELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.5%; Score 956.5; DB 8;
54.2%; Pred. No. 2.2e-82;
iive 55; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein of the invention SEQ ID NO:4209.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM05524 standard; protein; 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2002; 2002EP-00008400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 54.2*
Matches 179; Conservative
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BGS-42 polypeptide, cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antiinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
                                                           Ishii S;
k, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 DIDTSADAVEDLIEAEWEDLIQQYYSLVHGDAFISNSRNYFSQCQALLNRITSVNPQTDI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDT 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06731 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM0379-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNFE
                                                                                                                                                                            in gene therapy, regulating their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                           Otsuki T, Wakamatsu A, Sato H, Isł
Ho Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Indels
                                                                                                                                                                            New polynucleotides and polypeptides are useful in gene developing a diagnostic marker or medicines for regulatiexpression and activity, or as a target of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.1%; Score 944.5; DB 7; 54.3%; Pred. No. 2.8e-81; iive 55; Mismatches 86;
                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 4209; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :::| | :: | | : | | LIYKQGPAPNMQVSPERNAPLCPA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                             protein sequence of the invention.
                                                                            Hio Y, Otr
Otsuka M,
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                              (REAS-) RES ASSOC BIOTECHNOLOGY
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Best Local Similarity 54.3
Matches 176; Conservative
                                                             Sugiyama T,
                                                                              J, Isono Y,
Yoshikawa T,
                                                                                                                            WPI; 2003-723558/69.
N-PSDB; ADM03081.
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                                                             Isogai T, S
Yamamoto J,
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dermatological; tyrosine ligame modulator; gene therapy; tubulin ligase; tubulin-carboxypeptidase; cellular proliferation; reproductive disorder; testicular dancer; pulmonary disorder; lung cancer; gastrointestinal disorder; colon cancer; stomach cancer; neural disorder; brain cancer; liver cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; sepsis; acne; Sjogren's disease; scleroderma; human; HOTTL.
antibacterial; immunosuppressive; antiseborrheic;
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Homo sapiens.

WO2004005487-A2.

15-JAN-2004

09-JUL-2003; 2003WO-US021605

09-JUL-2002; 2002US-0394725P

(BRIM) BRISTOL-MYERS SQUIBB CO.

Nelson TC; Wu S, Feder JN,

WPI; 2004-099381/10.

New testie-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular disorders.

Disclosure; SEQ ID NO 5; 343pp; English.

This invention relates to a novel testis-specific tubulin tyrosine-ligase clike polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory cere, gastrointestinal-Gen, neuroprotective, endocrine-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, cantipatkinsonian, anitatkinitic, antiasthmatic, antiatkinity, antiasthmatic, antiasthmatic, neuroprotective, endocrine-Gen antibatkinsonian, anitatkinitic, antiasthmatic, antiasthmatic, antibatcherial, immunosuppressive, antiseborrheic or deractological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be useful for gene therapy. The BGS-42 polypeptide or polymucleotide can be cuseful condition in a subject, and for preventing, treating or apthological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, adsorder related to aberrant tubulin ligase activity, adsorder related to aberrant tubulin ligase activity, adsorder related to aberrant tubulin ligase activity, adsorders, testicular cancer, pulmonary disorders, carboxypeptides activity, adsorders, concer, stomach cancer, lung cancer, gastrointestinal disorders, concer, stomach cancer, carboxypeptide, polymucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS concers including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptide can be used as a preventive sequence is that of the human Control which is related to the invention. Note: The present control of the invention will but was obtained from

Sequence 292 AA;

Genbank.

DB 8; Length 292; Gaps 5; Indels Score 865.5; DB 8; Pred. No. 9e-74; 44; 30.3%; 58.7%; Conservative Similarity Best Local Sim Matches 159; Query Match Best Local S

133 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD 192

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180
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                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                  YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
193 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVOKYLKNDVGR
                                      SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 23727.
                                                                                                                    ELLWRQPVVEPPFSGSDLCVAGV-SVRRAR 398
                                                                                                                                241 ELIYKQPVTTSPASTPRPSCLLPMYSDTRAR 271
                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                        ABB65645 standard; protein; 992 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
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                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
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                                                                                                                                                                                                                                                                     Drosophila;
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Disclosure; SEQ ID NO 23727; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 992 AA;

51 LPGQLVDIACKVCQAYLGQLEHEDIDTSADAVED---LTEAEWEDLTQQYYSLVHGDAFI 25.3%; Score 722.5; DB 4; Length 992; 33.3%; Pred. No. 3.1e-59; ive 86; Mismatches 198; Indels 67; Matches 175; Conservative Similarity Query Match Best Local S

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                                                                 283 VIYPSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPV 342
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                                                                                                                                                                                                      343 TAQLCAQVQEDTIKVAVDRSCD----IGNFELLWRQPVVEPPPFSGSDLCVAGVSV---- 394
                                                                                                                                                                                                                                                     428
                                                                                                                                                                                                                                                                    678 NHGGGHGHYYYQQQRKERSLATSSVYRQRSAIIHPATSISRIHRAMPTFNATEYMEKYMV 737
                                                                                                                                                                                                                                                                                                 DPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESGGAAQPTRTKAAGKVELPACPCR 488
                                                                                                                                                                                                                                                                                                                 326 IPYSAIDFAYKRLVEYIDSCQHNDID-----FEDPPKIWEHDWDAFLFQHQQLVNEDGRI 380
                                                                                                               223 TORFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRGGRGAVWGS 282
                                   : | ::| | | | | | | | | | :::| | 381 QHDGGQRLEPMVKSCLSLVDKMKVHWPQYSLDGYQNMMIVKPANKCRGRGIILMDNLKKI
                                                                                                                                                                        ------RRARRQVLPVCNLKASASLLDAQPLKARGPSAMP------
                      SNS-----RNYFSQCQALLNRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEI
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Sequence 1688, Ap
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Sequence 1651, Ap
Sequence 167, App
Sequence 167, App
Sequence 41745, A
Sequence 2877, Ap
Sequence 2877, Ap
                                                                                                                                                                              Sequence 1, Appl.
Sequence 166, Appl.
Sequence 13181, A.
Sequence 13181, A.
Sequence 11197, A.
Sequence 11, Appl.
Sequence 1123242,
Sequence 116, Appl.
Sequence 116, Appl.
Sequence 2809, Appl.
Sequence 360042,
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Sequence 521157,
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Sequence 5, Appli
Sequence 147, App
Sequence 147, App
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APPLICANT: HESS, KENNETH R.
APPLICANT: HESS, MARK
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REFERENCE: UTXC:880US
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1684
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US-10-995-561-13381

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US-10-995-561-13381

US-10-995-661-13381

US-10-964-246-11

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US-10-624-932-7

US-10-624-932-5

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US-10-932-182A-167
US-10-750-185-41745
US-10-750-623-41745
US-10-1750-623-41745
US-10-821-234-64
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Matches:
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Sequence 43, Application US/10955054A

Publication No. US20050266420A1

GENERAL INFORMATION:
APPLICANT: PUSZTAI, LAJOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.37e-60
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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Score:
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Sequence 953009,
                                                                                                                               4, 2006, 09:58:51; Search time 4791 Seconds (without alignments) 450.890 Million cell updates/sec
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| SIDSS/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
| SIDSS/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                           OM protein - nucleic search, using frame_plus_p2n model
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US-09-925-065A-953009
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                                                                                                                                                                                                                                                                                                                                                                                                                         9263891 seqs, 1996499642 residues
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Database :

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Result Š.

Seguence 530109, Seguence 1143518, Seguence 353, App

Sequence 3, Appli Sequence 14615, A Sequence 3, Appli Sequence 3, Appl Sequence 14, App Sequence 58437, Sequence 58437,

Oy 381	1357 441 1411 461 1426 480 1479 490 1524	US-09-925-065A-953009/c Sequence 953009, Application US/09925065A ; Publication No. US20040181048A1 ; GENERAL INFORMATION: APPLICANT: Wang, David G. ; TITLE OF INVENTION: Identification and Mapping of Single ; TITLE OF INVENTION: Identification and Mapping of Single ; TITLE OF INVENTION: NUCLECTION POLYMORPHISMS in the Human Genome FILE REFERENCE: 10887.135 ; CURRENT APPLICATION NUMBER: US/09/925,065A ; CURRENT FILING DATE: 2000-10-80 ; PRIOR FILING DATE: 2000-11-20 ; PRIOR FILING DATE: 2000-11-30 ; PRIOR APPLICATION NUMBER: US 60/250,092 ; PRIOR APPLICATION NUMBER: US 60/261,766 ; PRIOR FILING DATE: 2001-01-30 ; PRIOR PILING DATE: 2001-01-30 ; PRIOR FILING DATE: 2001-05-09 ; RIUNG DATE: 2001-05-09 ; NUMBER: OF SEQ ID NOS: 957086 ; SCQ ID NO 953009 ; LENGTH: 666 ; TYPE: DNA ; ORGANISM: Homo sapiens	Alignment Scores: 6.16e-18 Length: 666 Pred. No.: 357.00 Matches: 106 Score: 106 Score: 46.4\$ Conservative: 22 Percent Similarity: 46.4\$ Conservative: 22 Best Local Similarity: 38.4\$ Mismatches: 61 Query Match: 612.5\$ 12.5\$ 14 BB: Gaps: 14 CS-10-635-977-2 (1-541) x US-09-925-065A-953009 (1-666) Qy 171 ProLeuSerArgAspAsnLysTrpValValGlnLysTyrlleGluThrProLeuLeulle 190
Best Local Similarity: 41.9\$ Mismatches: 128 Query Match: 32.3\$ Indels: 96 Bs: 12 12 Bs: 12 12 US-10-635-977-2 (1-541) x US-10-955-054A-43 (1-1684) Qy 73 GludspileAspThxSerAlaAspAlaValGluAspLeuThxGluAlaGluTxpGluAsp 92 1:: :: ::	Oy 112 nTyrPheSerGlnCysGlnAlaLeuAsnArglleThrSerValAsnBerArgAs 112 281 GACCTAGATGGAACACATGCTCTGATGCGAAGGGGCAGAACTCAGGCACTCGACC 337 Oy 112 nTyrPheSerGlnCysGlnAlaLeuLeuAsnArglleThrSerValAsnProGlnThrAs 132 113 pIleAspGlyLeuArgAsnIleTrpILelleLysProAlaAlaLysSerArgGlyArgAs 152 Db 338 CAGGGAGGGATCGTGAGGATCCTGAGGCGTGGAGCCTGGTACCGAGTAGA 397 Oy 132 pIleAspGlyLeuArgAsnIleTrpILelleLysProAlaAlaLysSerArgGlyArgAs 152 Db 398 CATGGAAGGGGATCTCTGGATCGTGAAGCCAAGTCCCGCGGAAGGG 457 Oy 152 pIleValCysMetAspArgAGIGLUGLIELeuGluLeuAlaAlaAlaAspHisProLe 172	Qy 212 pPherytleArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTr 212 Db 578 CACCAAGTTGACCTCAGACAGTGCTACTGGAACCCACTTACCGTG 637 Qy 212 pPherytlySGluSerTyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAs 232 Db 638 GTTCTACCGCAGCTGTTATCCACCGCAGCCTTCCCTGGAACCTGGA 697 Qy 232 pSerProLeuLeuProAlaHishanAsnAshalaValGlnLyrLeuLysAsnAspValGlyAr 252 Db 698 CAACTCAGTGCACCTGTGCAACTCCATCCAGAGCACTTGTCATGCCATCG 757 Qy 252 gSerProLeuLeuProAlaHishanMeTTrpThrSerThrArgPheGlnGluTyrLeuGl 272 Db 758 GCATCCACTGCACACACTCCATCCAGAGCACTGGAGACTCAGGCCACTGCA 817 Qy 272 nArgGlnGlyArgGlyAlaValTrpGlySerValIleTyrProSerMetLysLysAlail 292 Db 318 GGAGTGCCCCACAATGTCGTCACCACATCGTGCTGGCATGAGGATGCTGCA Qy 272 nArgGlnGlyArgGlyAlaValTrpGlySerValIleTyrProSerMetLysLysAnlail 292 Db 312 uTyrGlyAlaAspDheAtGCTTGGTCCACCATCATCGTGCTGGCATGAGATGTGGATGTTGGATTTGAGCTGTGTTTGAGCTCCACCATCATCGTGCTGCTGTTTGAGATTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCTTTTGAGCT	Oy 332 rSerProThrMetHisProSerThrProValThrAlaGhnLeuCysAlaGhnValGhGl 352

; APPLICANT: SEKI, NAOHIKO ; APPLICANT: YOSHIKAMA, TSUTOMU ; APPLICANT: OTSUKA, MOTOYUKI ; APPLICANT: NACAHARI, KEMII ; APPLICANT: NACAHARI, KEMII ; APPLICANT: NASUHO, YASHHIKO ; TITLE OF INVENTION: Novel full length cDNA ; FILE REFERENCE: 084335-0191 ; CURRENT APPLICATION NUMBER: US/11/072,512 ; CURRENT APPLICATION NUMBER: US 60/350,978 ; PRIOR FILING DATE: 2002-01-25 ; PRIOR FILING DATE: 2001-015 ; RIOR FILING DATE: 2001-015 ; RIOR FILING DATE: 2001-015	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 1688 ; LENGTH: 2624 ; TYPE: DNA ; ORCANISM: Homo sapiens	-11-072-512-1688 fed. No.: 3.43e-13 octs: 302.00 rcent Similarity: 24.0% ery Match: 10.6%	US-10-635-977-2 (1-541) x US-11-072-512-1688 (1-26	Qy 82 ValGluAspLeuThrGluAlaGluTrpGlu	Qy 92AspLeuThr	Qy 98 TyrSerLeuValHisGlyAspAlaPheIleSerAsn	Qy 118 GlnAlaLeuLeuAsnArgIleThrSerValAsn ::: ::: Db 627 GAGCGTGAGGCAGGAAGCTGGAGGCAGCCAAGTGT	Qy 132AspIleAspGlyLeu. ::::: Db 687 ATGCCTTGCGAGTACCACCTGTTTGTAGAGAGTTT	Oy 141 IleIleLysProAlaAlaLysSerArgGlyArgAsp	Qy 161 GluIleLeuGluLeuAlaAlaAlaAspHisProLeuinneuinneuinneuinneuinneuinneuinneuin	Db 864 CCCGTGGAGAACTATGTGGCTCAGCGTTACATTGAA	Qy 194 LysPheAspIleArgGlnTrpPheLeuValThrAsp'	Oy 214 TyrLysGluserTyrLeuargPheserThrGlnargi	Qy 234 AlaileHisLeuCysAsnAsnAlaValGlnLysTyrl :::
	238 CygasnasnalaValGlnLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuPro 		300 GCCCAGCCCAC	<pre>Qy 318 ValLeuGlyArgAspPheArgProTrpLeulleGluIleAsnSerSerProThrMetHis 337 </pre>	Oy 338 ProSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIleLysVal 357	Oy 358 AlaValAspArgSerCysAspIleGlyAsnPheGluLeuLeuTrpArgGlnProValVal 377	Qy 378 GluproProProPheSerGlySerAspLeuCysValAlaGlyValSerValArgAla 397	Oy 398 ArgArgGlnValLeuProValCysAsnLeuLysAlaSerAlaSerLeuLeuAspAlaGln 417	Oy 418 ProLeuLysAlaArgGlyProSerAlaMetProAspProAlaGlnGly 433	RESULT 3 US-11-072-512-1688 i Sequence 1688, Application US/11072512 i Publication No. US20060029945A1 i GENERAL INFORMATION i ADDITORMATION i ADDITORMATI	; AFFLICANT: ISOGAL, TAKAO APFLICANT: SIGIYAMA, TOMOYASU APFLICANT: OTSUKI, TETSUJI	APPLICANT: WAKAMATSU, AI APPLICANT: SATO, HIROYUKI APPLICANT: ISHIJ, SHIZUKO APPLICANT: VAMAMOTO, IIN-ICHI	ISONO, YUUKO HIO, YURI OTSUKA, KAORU NAGAI KETICHI	

A-----CAG 1001 ACTGGTGTGACGTCAGCTGGCTCCGG 506 rgcggatcactrccggaaccac 566 SINGERARGASHTYRPHESERGINCYS 117 ------ProGlnThr----- 131 |||:::||| stgacttcttccccaaaacctttgag 686 uArgAsn------IleTrp 140 pijevalCysMetAspArgvalGlu 160 |||| |CATCTTCCTCTTCCGTAGGCTGAAG 806 uThrProLeuLeulleCysAspThr 193 TCGCAAAACCCAGGAATCACCTGG 746 userArgAspAsnLys----- 177 pTrpAsnProLeuThrileTrpPhe 213 G-----GTG 962 gPheSerLeuAspLysLeuAspSer 233 rLeuLysAsnAspValGlyArgSer 253 2624 132 76 200 144 23 ive: 2624)

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APPLICANT: 1SOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
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APPLICANT: ISONO, JUN-ICHI
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APPLICANT: HIO, YUKI
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OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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NAGAI, KEIICHI
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                             254 ProLeuLeuProAlaHisAsn-------MetTrpThrSerThrArgPheGln 268
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                                                                           PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: UP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1401
                                                                                                                                                                                                                                                                                                                                                                                                           Length:
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
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Sequence 1401, Application US/11072512

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741 CCTGGAGGACCTC-----CCGTGG-----
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APPLICANT: YOSHIKWA, TSUTOWU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVel full length cDNA
FILE REPERENCE: 084335-0191
CURRENT FILING DATE: 2005-03-07
PRIOR PELICATION NUMBER: US 60/350,978
PRIOR PELICATION NUMBER: UP 2001-379298
PRIOR PILING DATE: 2002-01-25
PRIOR PELING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VOS: 4096
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                                                                                                 OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-1651
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Best Local Similarity:
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541 CAAGCTTACCAGGAAAGACTGTTTGGCCAAACACCTGAAGGCACATGAGGAGGATGTATGG 600
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          GlnTyr------TyrSerLeuValHisGlyAspAlaPhelleSerAsnSer 110
                                                                                                             CGAACA-----CAACAGTGTTAAACCGTGGCAGCAGCTAAACCACCCCCGGAACCAC 540
                                                                                                                                                                                                                                                                                                         661 CGTGGCTGAATACTTTCAGGAGAGGCAGATGCTGGGCACCAAGCATAGCTATTGGATTG 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 rThrGlnArgPheSerLeuAspLysLeu---AspSerAlalleHisLeuCysAsnAsnAl 241
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                                                                                                                                                                                                                                                                                --------GlnThrAsp-IleAspGlyLeuArgAsnIleTrpileIl
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                                                                                                                                               GlnAlaLeuLeuAsnArgIleThrSerValAsnPro----
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Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                             ArgAsnTyrPheSerGlnCys-
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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795

Query Match: 5.1% Indels: 83 DB: 9 Gaps: 10	-635-977-2 (1-541) x US-10-932-182A-167 (1-2250)	Qy 94 ThrGlnGlnTyrTyrSerLeuValHisGlyAspAlaPheIleSerAsnSer 110 	111ArgAsnTyrPheSerGlnCysGlnAlaLeuLeuAsnArgIleThr	1324	Qy 126 SerValAsnProGlnThrAspIleAspGlyLeuArgAsnIleTrpIleIleLysProAla 145 ::: ::: ::: ::: ::: Db 1384 GAGTTACGTCAAGAATTGGAAAAGGAAAGGCAAATGGTGGATTGTGAAACCAAGT 1443	Qy 146 AlaLysSerArgGlyArgAspIleValCysMetAspArgValGluGluIleLeuGluLeu 165	Oy 166Ala 166	Qy 181 GlnLysTyrileGluThrProLeuLeulleCysAspThrLysPheaspile 197	Oy 198 ArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSer 217	Qy 218 TyrLeuArgPheSerThrdlnArgPheSerLeu 228	Qy 229 AspLysLeuAspSerAlaileHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsn 248	Qy 249 AspValGlyArgSerProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGln 268	Oy 269 GluTyrLeuGlnArgGlnGlyArgGlyAlaValTrpGlySerValIleTyrProSerMet 288 ::: Db 1885 TCCCTAGAAGAAATTCCAAACGAG 1908		296 MetLysValAlaGlnAspHisValGluProArgLysAsnSerPheGluLeuTyrGlyAla :::	316 AspPheValLeuGlyArgAspPheArgProTrpLeulleGlulleAsmSerSerProThr	336 MetHisProSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIle	Qy 356 LygValalaVal 359	Db 2149 AAGTATTGTGTT 2160
1564 AATGCGGAATTCATGGATAATAACAAAGTAAATATCTCCCCAATTGCGCCACTTTATCATA 1	OY 181 GIALLYSTYTILGGLUThrProLeuleulleCysAspThrLysPheAsp1le 197	198 ArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSer	GGGATTTACAAGTATTCGTATACGATG	27 210 LYLBOALDANDELLINEATHERTRESTERNOOT	Qy 229 AspLysLeuAspSerAlaIleHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsn 248	249 AspValGlyArgSerProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGln	269 GlufyrLeuGlnArgGlnGlyArgGlyAlaValTrpGlySerValIl	DD 1969 FARANCHISANALITARGARCAGATICATIGCATARCAARIGAGGITTICTTAGGGGCA 1968 QY 296 MetLysValAlaGlnAspHisValGluProArgLysAsmSerPheGluLeuTyrGlyAla 315 DD 1969 GTAAATGTAAACAGGTAAAGTTTCAAAACGTTAACAAAATGAGTTAAAAAAAA	316 AspPheValLeuGlyArgAspPheArgProTrpLeulleGlulleAsnSerProThr	336 MetHisProSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIle		RESULT 7 US-10-912-182A-167	; Publication No. US20060046253A1 ; GENERAL INFORMATION: ; APPLICANT: NAKAO, YOSHIHIRO	; APPLICANT: NALAWAY, YUKIKO ; APPLICANT: FUDIMURA, TOWOKO ; APPLICANT: FUJIMURA, TOSHIHIKO	; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS; FILE REFERENCE: 030685-043; CURRENT APPLICATION NUMBER: US/10/932,182A; CURRENT FILING DATE: 2004-09-02	; NUMBER OF SEQ ID NOS: 197023 ; SCFWARR: PatentIn version 3.3 ; SEQ ID NO 167 ; LENGTH: 2250	; TYPE: DNA ; ORGANISM: Saccharomyces pastorianus US-10-932-182A-167	lent Scores: 0.253 Length: 2250	Score: 144.50 Matches: 65 Percent Similarity: 36.1% Conservative: 52 Best Local Similarity: 20.1% Mismatches: 124

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TYPE: DNA
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---GACAACCAAGGCCAGATGCACGTGATCCAGAAATACCTGGAGGTCCCGTTGTTCTG 194
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                                                                       APPLICANT: MIT GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: MIT SERR, Richard
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Domis
APPLICANT: BANTIN, Domis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VETSION 3.1
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CTCATCTTCTCAGAAGCTACAGAACTGTTGGATTTCATA-----
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Matches:
Conservative:
Mismatches:
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Sequence 41745, Application US/10750623

PUBLICATION NO. US20050287531A1

GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David
                            Sequence 41745, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     GRGANISM: Bovine 19866880883232
US-10-750-185-41745
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141.00
49.2%
31.0%
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Best Local Similarity:
RESULT 8
US-10-750-185-41745
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 41745
LENGTH: 1319
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Sequence 2877, Application US/11124368A
Sequence 2877, Application US/11124368A
Publication No. US2050287559A1
GRNERAL INFORMATION:
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FAURIN, Demnis
TITLE OF INVERTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TITLE OF INVERTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALEGRIIN VERSION 3.1
SEQ ID NO 41745
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PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bovine 19866880883232
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6660 GAGCGGAAGCATGAAAGGATAGGAAAAAAACCAACCTCCTATACACACAC	264 SerThrArgPheGln 268	::: 6600 CCTTCTCTTTCTCTCTCTTAGGACCCCAAGAAACTAAGACCCGATGATAAAATTCACT 654	269 GlufyrLeuGlnArgGlnGlyArgGlyAlaValTrpGlySerValIleTyrPro 286	TTGGAGAATCTACTGGTTACTAATTGAAGAC	287 SerMetLysLysAlaIleAlaHisAlaMetLysValAlaGlnAspHisValGluProArg 306		THE THE THE THE THE THE THE THE THE THE	<pre>307 LysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGlyArgAspPheArgProTrp 326 </pre>	6420 AATAAC	327 LeuileGlulleAsnSerSerProThrMetHisProSerThrProValThrAlaGlnLeu 346	::::: 6414 TTCATAAAGTTAAAGAGCTTCCATCCCTTCAC	347 CysAlaGlnValGlnGluAspThrIleLysValAlaValAspArg 361	 	362 SerCysAspileGlyAsnPheGluLeuLeuTrvAraGlnProValValGluProPro 381	Gecceccestrates				GGGACCGGAAAAGCAGAAGCTCAGCGCGAACCGACGGGGGGTTCCGCGGCGCAGTGCG	408 LysAlaSerAlaSerLeuLeuAspAlaGlnProLeuLysAla 421	22Ardio Version 1	GCGCCCGCCCCGGCCCAGCTGGCCCGCACGGCGTGCCCCCGAGCGAG			GluLyBGlyLeuProLeuAlaLeuLeuAlaProLeuArgGlyAlaAlaGluSerGlyGly		468 AlaAlaGlnProThrArgThrLysAlaAlaGlyLysValGluLeu 482		483 ProAlaCysProCygArgHisValAgpSerGlnAlaProAsnThrGlyValProValAla 502	ı	503 GlnProAlaLvsSerTrnAspProAsnGlnLenAsnAlaHisProLenGlnDroValLen 522		A ** A **	523 Argeryteurysiniatacrootyare 533 	11	US-10-821-234-64/c ; Sequence 64, Application US/10821234
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SE	LENGTH:	TITE: DAM TOWNISM: Homo mapiens FRATIDE:	NAME/KEY: misc_feature	LOCATION: 4805, 4806, 4807, 4808, 4809, 4810, 4811, 4812, LOCATION: 4815, 4816, 4817, 4819, 4819, 4820, 4821, 4822,	LOCATION: 4835, 4836, 4837, 4838, 4839, 4841, 4842, 4843,	OTHER INFORMATION: n = A,T,C or FEATURE:	NAME/KEY: misc_feature	LOCATION: 4854, 4855, 4856, 4857, 4858, 4859, 4860, 4861,	LOCATION: 4864, 4865, 4866, 4867, 4868, 4869, 4870, 4871, 4872, 4 LOCATION: 4874, 4875, 4876, 4877, 4878, 4879, 4880, 4881, 4882	RMATION: n = A,T,C or G	Y: misc feature	LOCALION: 4003, 4004, 4003, 4006, 4007, 4008,	, 4908, 4909, 4910, 4911, 4 , 4918, 4919, 4920, 4921	FEATURE:	misc_feature : 4922, 4923, 4924, 4925, 4926, 4927, 4928, 4929, 4930, 4	4935, 4936, 4937, 4945, 4946, 4947,	4955, 4956, 4957, 4958, 4959, 4 cor G		4961, 4962, 4963, 4964, 4965, 4966, 4967, 4968, 4971, 4972, 4973, 4974, 4975, 4976, 4977, 4978,	4984, 4985, 4986, 4987, 4988, 4989, 4994, 4995, 4996, 4997, 4998, 4999	 misc feature 5000, 5001, 5002, 5003, 5004, 5005, 5006, 5007, 5008,	LOCATION: 5010, 5011, 5012, 5013, 5014, 5015, 5016, 5017, 5018, 5019, LOCATION: 5020, 5021, 5022, 5023, 5024, 5025, 5026, 5027, 5028, 5029,	LOCATION: 5030, 5031, 5032, 5033, 5034, 5035, 5036, 5037, 5 OTHER INFORMATION: n = A,T,C or G	99	Length:	136.50 Matches: 89	simitatity: Zi./* Mismacches: : Indels:	14 Gaps:	-IO-035-977-2 (I-541) X US-II-124-368A-2877 (I-47460)	PheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSerTyrLeu	6840 T.	220	TGTAAAAAT	233	Db 6720 AGGCTACTGGCTAGCGATGGGTTTGGCGCTGACTTAAAATAATCTTGCTAGAAAATG 6661	Oy 246 LeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsnMetTrpThr 263

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390 AlaGlyValSerValArgArgAlaArgArgGlnValLeuProvalCysAsnLeuLysAla 409
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                                               116 CTGTGGCTCCTGTCGCCACACAGTCTCTGCCGCGGCTCCCG--
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Sequence 1, Application US/11219995
Publication No. US20060003379A1
GENERAL INCRNATION:
APPLICANT: Miyazono, Kohei
APPLICANT: Miyazono, Kohei
APPLICANT: Mashaliro
FILE REFERENCE: L0461.70148US01
CURRENT APPLICATION NUMBER: US/11/219,995
CURRENT APPLICATION NUMBER: US/11/219,995
CURRENT APPLICATION NUMBER: US/10/390,553
PRIOR FILING DATE: 2003-09-17
PRIOR FILING DATE: 2001-08-07
PRIOR FILING DATE: 1998-06-13
PRIOR FILING DATE: 1998-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NOS: 10
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                GENERAL INFORMATION:
APPLICANT: Labat. Ivan
APPLICANT: Adarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT FILING DATE: 2014-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PLILNG DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL-SEQ_genes Version 1.0
SEQ ID NO 64
LENGTH: 10373
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OTHER INFORMATION: n = a,t,c or
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Publication No. US20050255114A1
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ORGANISM: Homo sapiens
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Pred. No.:
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Qy 324 ArgProTrpLeuIleGluIleAsnSerSerProThrMetHisProSerThrProVal 342	ProPheSerGlySerAspLeuCysValAlaGlyValSerValArgArgAlaArgArgGln	406 AsnLeuLysAlaSerAlaSerLeuLeuAspAlaGInProLeuLysAlaArgGlyProSer	Db 1354CCACCACCGCCGCTGCCCCCTCGCCTCCCTCACCTCTCACACTGT 1410 Qy 466 GlyGlyAlaAlaGlnPro	RESULT 14 US-11-136-527-1889 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136527 Sequence 1889, Application US/11136 Sequence 1889, Application US/11136 Sequence 1889, Application US/11/136 Sequence 1889 Sequence 1880 Sequence 1
Oy 410 SerAlaSerLeuLeuAspAlaGlnProLeuLysAlaArgGlyProSerAlaMetProAsp 429	Qy 467GlyAlaAlaGln	51 76 52 70	RESULT 13 US-10-330-773-662 i Sequence 662, Application US/10330773 j Sequence 662, Application US/10330773 j Publication No. US20060040262A1 j GENERAL INFORMATION: APPLICANT: David W. Morris APPLICANT: David W. Morris APPLICANT: Marc Malandro FILE OF INVENTION: Novel Compositions and Methods in Cancer FILE REPERENCE: 529425001300 CURRENT APPLICATION NUMBER: US/10/330,773 CURRENT FILING DATE: 2002-12-27 j NUMBER OF SEQ ID NOS: 981 j SOFTWARE: FastSEQ for Windows Version 4.0 j SEQ ID NO 662 j LENGTH: 2754 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA USGADAISM: MUS musculus US-10-330-773-662	Alignment Scores: Pred. No.: 126.50 Matches: 784 Score: 126.50 Matches: 78 Score: 126.50 Matches: 78 Score: 126.50 Matches: 78 Score: 126.50 Matches: 15 Best Local Similarity: 29.4\$ Conservative: 15 Ouery Match: 4.4\$ Mismatches: 110 Ouery Match: 9 Gaps: 133 US-10-635-977-2 (1-541) x US-10-330-773-662 (1-2754) Cy 264 SerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGlyAlaValTrpGlySerVal 283 :::

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Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Sequence 13381, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

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CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS DETECTION AND USES THEREOF
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  TITLE OF INVENTION: CARDIOVASCULAR DISORDER:
TITLE OF INVENTION: DETECTION AND USES THERE;
FILE REPERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRASELSEQ for Windows Version 4.0
SEQ ID NO 13381
LENGTH: 14248
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CORGANISM: Homo sapiens
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Title:

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US-10-615-659-1

Sequence 1, Application US/10615659

Sequence 1, Application US/10615659

Publication No. US20040157234A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: PROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: D0283 NP

CURRENT APPLICATION NUMBER: US/10/615,659

CURRENT APPLICATION NUMBER: US. 60/394,725

PRIOR APPLICATION NUMBER: U.S. 60/394,725

PRIOR FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 102

SEQ ID NO 1

SEQ ID NO 1
                                                                                                                                                                                                                       Sequence 494, App
Sequence 494, App
Sequence 199, App
Sequence 199, App
Sequence 1766, Ap
Sequence 4121, Ap
Sequence 2315, Ap
Sequence 24894, A
Sequence 24894, A
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Sequence 7660, Ap
Sequence 7660, Ap
Sequence 2032, Ap
Sequence 5962, Ap
Sequence 5187, Ap
Sequence 135929,
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Sequence 23414, A
Sequence 23413, A
                                                                      Sequence 631, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 39, Appli
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Sequence 2016, Ap
Sequence 1971, Ap
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Sequence 135927,
Sequence 135927,
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US-10-615-679-3
US-10-615-679-39
US-10-102-86-199
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ORGANISM: Homo sapiens
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-Q=/abss/ABSSWEB spool/US10635977/runat 04042006 103543_10259/app_query.fasta_1
-NATRIX-blosum62 - LOOPEXT=0 - LOOPEXT=0 - TAR SCORE=pct
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-HEAFSIZE=500 - MINLEN=0 - MAXIN=200000000 - HOST=Abss07
-USER=US10635977 @CGN 1 1 1026 @runat 04042006 103343 10259 - NCPU=6 - ICPU=3
-NO MMAP - NEG SCORES=0 -WAIT - DSPBLOCK=100 - LONGLOG - DEV TIMEOUT=120
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1: /cgn2_6/ptodata/1/pubpua/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpua/USO9_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpua/USO9A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpua/USO9A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpua/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpua/US10A_PUBCOMB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                              nucleic search, using frame_plus_p2n model
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YGAPOP=10 Database :

Result No.

DB DB

Minimum | Maximum |

Searched:

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US-10-835-9//-1

Sequence 1, Application US/10635977

Publication No. US20040171131A1

GENERAL INFORMATION:

APPLICANT: Bristol-IMyers Squibb Company

TILLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TILLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TILLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TILLE OF INVENTION: TOORSHE: 105/10/635,977

CURRENT APPLICATION NUMBER: U.S. 60/394,725

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

PRIOR PRICH OF TESTIS 2003-07-09

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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                                                               ArgSerCysAsplleGlyAsnPheGluLeuLeuTrpArgGlnProValValGluProPro
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                                MetalaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArg
                                              ATGCCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGCAGCAGCAGAA
                                                                            SerLysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAsp
                                                                                           AGCAAGCCCAGGGACCCAGAGGAGGAGGCCGGGAGCACCTGAGCAGCAGCAAGAT
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381 ProPheSerGlySerAspLeuCysValAlaGlyValSerValArgArgAlaArgArgGln 400 1140	0y 441 ArgAspLeudlyLeuLysGludluLysGlyLeuProLeuAlaLeuLeuAlaProLeuArg 460	Db 1440 GAGCTCCCGGCCTGTCGCCACGTGGACAGTCAGGCCCCAAACACCGGTGTCCCC 1499 Oy 501 ValalacInProAlaLysSerTrpAspProAsnGInLeuAsnAlaHisProLeuGluPro 520	RESULT 6 US-10-635-977-10 Sequence 10, Application US/10635977 Publication No. US20040171131A1 CENERAL INFORMATION: TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42 FILE REFERENCE: D0283A CIP	CURRENT APPLICATION NUMBER: US/10/635,977 CURRENT PILING DATE: 2003-00-07 PRIOR PILING DATE: 2002-07-09 PRIOR FILING DATE: 2002-07-09 PRIOR FILING DATE: 2003-07-09 NUMBER OF SEQ ID NOS: 103 SOFTWARE: Patentin version 3.2 SOFTWARE: Patentin version 3.2 LENGTH: 1859 TYPE: DAA ORGANISM: Homo sapiens	ignment Scores: 1.52e-270 Length: 1859 d. No: 2698.50 Matches: 522 orent Similarity: 96.5\$ Conservative: 0 st Local Similarity: 96.5\$ Mismatches: 4 ery Match: 7 Gaps: 2 10-635-977-2 (1-541) x US-10-635-977-10 (1-1859)	Qy 1 MetalaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArg 20
ATGGCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGAAACCCAGCACAAGAAGCCAGCAGCAG	227 AAGGTGTGCCAGGCCTACTGGGGCCAGGTGGAGCATGGACATGGACATGGCAGAT 286 81 AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu 100 81 AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu 100 81 AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlll	CTGAATAGAATCACGTCTGTGAACCCTCAGACGGCATTGACGGCCTCCGGAACATCTGG T1eIleLysProAlaAlaLysSerArgGlyArgAspIleValCysMetAspArgValGlu	181 GinLysTyrInGluThrProteuLeulleCyBabPIThrLysPheapplieargGinTip 200	AlavalGlnLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsn	301 Applia VALGIUFPOATGLYSABLSETPROGLULEUTVELYALASPERASPERASPERASPERASPERASPERASPERASPER	361 ArgSerCyBAsplleGlyAsnPheGluLeuLeuTrpArgGlnProValValGluProPro 380

191 ProPheSerGlySerAspLeuCysValalaGlyValSerValArgArgAlaArgCln 400	Oy 521 ValLeuArgGlyLeuLysThrAlaGluGlyAlaLeuArgProProGlyGlyLysGly Db 1560 GTGCTGCGGAGCCTGAAGACAGCGGGGGTGCGCTGCGCGCGGGGAAAAGGT 1619 Oy 541 Ser 541 Db 1620 TCA 1622 RESULT 7 US.10-615-659-11 SEQUENCE 11, Application US/10615659 Publication No. US20040157234A1 SEQUENCE 11, Application US/10615659 Publication No. US20040157234A1 SERBULT 7 US.10-615-659-11 SEQUENCE 11, Application US/10615659 Publication No. US20040157234A1 SERBULT 7 US.10-615-659-11 SEQUENCE 11, Application US/10615659 PUBLICATION NUMBER: US/10/615,659 CURRENT APPLICATION NUMBER: US. 60/394,725 PRIOR PRILOR PILING DATE: 2002-07-09 PRIOR PILING DATE: 2002-07-09 PRIOR PILING DATE: 2002-07-09 SOFTWARE: PatentIn version 3.2 LENGTH: 3465 COGRANISM: Homo sapiens US-10-615-659-11	Alignment Scores: Alignment Scores: Pred. No.: 2693.00 Matches: Score: Best Local Similarity: 95.4\$ Mismatches: 1.36e-269 Matches: 516 Conservative: 0 Mismatches: 3 Mismatches: 3 Query Match: 7 No.10-635-977-2 (1-541) x US-10-615-659-11 (1-3465) Qy 1 MethalserSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArg Qy 1 MethalserSerIleLeuLysTrpValValValIl
21 SerLysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAsp 40 107 AGCAAGCCCAGGGAGGAGGCCGGGAGCCACCTCAGCCACCAGCCAAGAT 166 41 AlaGluAsnAlaGluAlaLysLeuArgGlyLeuProGlyGlnLeuValAspIleAlaCys 60 167 GCTGAAAATGCTGAGGCTCAGGGCCCTCCCGGGGCAGCTTGTGGACATCGCGTGC 226 61 LysValCysGlnAlaTyrLeuGlyGlnLeuGlyHisGluAspIleAspThrSerAlaAsp 80 61 LysValCysGlnAlaTyrLeuGlyGlnLeuGlyHisGluAspIleAspThrSerAlaAsp 80 627 AAGTGTGCCAGGCCTACCTGGGGCCTCTCGGGGCATCGACACAGCAGTAGAGAT 286 81 AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu 100 64 AlaValGluAspAlaPheIleSerAsnSerArgAsnTyrPheSerGlnCysGlnAlaLeu 120 65 CCGTGGAGGACCTCACTGAGGCCGAGTGGAGACCTCAGCAGATACTCCCTC 346 66 CCGTGGAGGACCTCACTGAGGCCGAGTGGAGACCTCAGCAGATACTCCCTC 346 67 GCCGTGGAGGACCTCACTGAGGCCGAGTGGAGACTTGAGGCTCCGGAACATCTG 363 68 GCCGTGGAATAGAATCACGTCTGGAACCCTCAGACGCCCGGAACATCAGCGCCCGGAACATCGAGGCCCGGAACATCGAGGCCCGAGACACAACTCCAGAGCCCCGAGACCCCGAGACACAACTCCAGAGCCCCGAGACCCCGAGACCCCGAGACACAACTCCCAGACCCCGAGACACAACTCCCAGACCCCGAGACACAACTCCCAGACCCCGAGACACAACTCCCAGACACAACTCCAACAACTCCCAGACACAACTCCCAGACACAACTCCAACACACAC	GlulleLeuGluLewalaalaalaaAspHisProLeuSerArgAspAsnLysTrpValVal GGGGACCTGGAGCTGCAGCCCCTCTTTCCAGGGACAACAAGTTGGGTGC GlnLysTyrIleGluThrProLeuLeuIleCysAspThrLysPheaspIleArgGluTrp CAGAAGTACATCGAGACCCGCTGCTCATCTGTGACCAGGACAACATCGACATCGAGATGGG PheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSerTyrLeuArg	301 AspHisValGluProArgLySAsnSerPheGluLeuTyrGlyAlaAspPheValleuGly 320 301 AspHisValGluProArgLySAsnSerPheGluLeuTyrGlyAlaAspPheValleuGly 320 302 GACCACGTGGAGCTTCGCAAGACGCTTTAGGCTTACGGGGCTGATTCGTCCTTGGG 963 321 ArgAspPheArgProTrpLeu1leGluIleAsnSerSerProThrMetHisProSerThr 340

	Oy 1 MetalaSerSerIleLeuLySTrpValValSerHisGlnSerCysSerArg 20
138 AGCAMACTCANGGGACGANGCACCGGGACCTGANGCACGGCACACT 197 13. Alacinamalacius 197 1	361 ArgSerCysAsplleGlyAsnPheGluLeuLeuTrpArgGlnProValValGluProPro 380 [

0y 401 ValLeuProValCyshsnLeuLyshlaSerAlaSerLeuLeuAspAladlnProLeuLys 420 0y [3231 TCA 3211 TCA 10-615-659-9 Sequence 9, Appl Publication No. Publication No. TITLE OF INVENT FILE REFERENCE: CURRENT FILING PRIOR PELICA CURRENT FILING PRIOR	Alignment Scores: Pred. No.:
AlaGluAsnalaGluAlaLysLeuArgGlyLeuProGlyGlnLeuValAspIlealaCys GCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGACATCGCGTGC LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAsp	181	301 AspHisValGluProArgLysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGly 320 [

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Sequence 9, Application US/10635977
; Sequence 9, Application No. US2004017131A1
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; GENERAL INFORMATION:
    TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
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; TITLE OF INVENTION: POLS3A CIP
; CURRENT APPLICATION NUMBER: U.S. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR APPLICATION NUMBER: U.S. 10/615,659
; NUMBER OF SEQ ID NOS: 103
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                                                                                                                                                                    ValAlaGlnProAlaLysSerTrpAspProAsnGlnLeuAsnAlaHisProLeuGluPro
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                                                                      MetTrpThrSerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGlyAlaValTrp
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GCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGACATCGCGTGC
                                    ValHisGlyAspAlaPheIleSerAsnSerArgAsnTyrPheSerGlnCysGlnAlaLeu
                                                                                                                                    GTTCATGGGGATGCTTTCATCTCCAATTCAAGAAATTACTTTTCGCAGTGCCAGGCTCTG
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                        LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAsp
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Qy 421 AlaArgGlyProSerAlaMetProAspProAlaGlnGlyProProSerProAlaLeuGln 440 Db 1346 GCAGGGCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	RESULT 11 US-10-723-860-631/c ; Sequence 631, Application US/10723860 ; Sequence 631, Application US/10723860 ; Beducation No. US2004025366A1 ; GENERAL INFORMATION: ; APPLICANT: AIZ: Natasha ; APPLICANT: Ginsburg, Wendy M. ; APPLICANT: Zlotnik, Albert ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators ; TITLE OF INVENTION: WINDER: US/10/723,860 ; CURRENT APPLICATION NUMBER: US/10/723,860 ; RIOR APPLICATION NUMBER: 2003-11-26 ; PRIOR FILING DATE: 2002-11-26 ; NUMBER OF SEQ ID NOS: 8393 ; SOFTWARE: PatentIn Version 3.2 ; LENGTH: 101270 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-723-860-631	Alignment Scores: Alignment Scores: Bred. No.: Score: 1.18e-174 Matches: 438 Percent Similarity: 32.24 Matches: Best Local Similarity: 32.14 Mismatches: 3 Query Match: B.
61 LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAsp 80	PheLeuvalThrasptrpasnProLeurill	Argaspheargprofrocadacactricagcrctacacacacacacacacacacacacacacacacacac

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ò	151 151	Db 45903 CGGTGGGCGACCTGGACACCTCGGGCCAGGGAATGGGCTGCTGCTGCATGCCTGGAGCA 45844
дg	46983 GGACAGTITCAGGCCCACAGCACCACAGGAAGGAAGGAGGAGGAGCAGAACGCCGAGGCA 46924	
ò	!	Db 45843 GCGGCAGTGAGAAGCAGCACGGGCAGCCCCTCACTGCCACCTGCCACGAGAGGC 45784
QΩ	46923 GGCGTGGGGGTCAGGACTCAGGCGCTGGAGGCTGGAGGCGTCTTCACAGCATGTGT 46864	Qy 232 232
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qq	46863 TCCGATCACAGGCAGGATCCGGGTTGATGGGTTAATCAGGATTTCCTCCTTTGTATTCA 46804	Qy 232 232
λŏ	! !	Db 45723 CACCGGCCTTCAAAGCCAGCGCCCTACACCCCACGCTCTGTGCATCATCTCTGGAAAATC 45664
පු	46803 CAAACTGGTCTATGCTTTCCTTTTTAGTTTTTTTTTTTT	Qy 232 232
ò		Db 45663 TIAAAAGGCACCATITIGCCTGTGCCCAGGGGATTGGAATGGTGGGCAGCACCTGGG 45604
qa	46743 TGAAACGGAGTTTCACTCTTGTTGCCCAGGCTGAAGTGCAGTGGCGCAATCTTGCCTCAC 46684	Qy 232 232
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qq	46683 TGCAACCTCCACCTTCCAGGTTTAAGCAATTCTCCTGCCTTAGCCTCCCAAGTAGCTGGG 46624	
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qq	46623 ACTACAGGCGCCCACCACACGCTAATTTTTGTATTTTTAGTAGAGATGGAGTTTCA 46564	Qy 232 232
δŏ	151 151	Db 45483 GAGCCTGTGGAGTCCTCAGGAGTGTGCTGTGCACACAGGGACGCCTGCCACCCTCTGTCT 45424
qq	46563 CCATGITGGCCAGGCTGGTCTTGAACTCCCGACCTCAAGTGATTCACCTGGCCTCGGCCTC 46504	Qy 232 232
ò	!	Db 45423 GCACCAAGGCTTCCTCTGACTATTGTGGGCCCTTGCTTGGTGAGGCGCTAGGGGACC 45364
ф	46503 CCAAAGTGCTGGGATTACAGGCATAAGCCACCATGCCCATCCTCTGGCTCCCTTTTAAA 46444	Qy 232 232
ò	151 151	Db 45363 TGACGCTGGGCAGGAAGGGGGTCTGCTTTTTACGAGTGAGAATCCAGGGAGGCCTGAGA 45304
Ор	46443 AGTGTCTCTGTCCCTTCCCTTCACTGATCTCTGTGTCCCCTCTGGGGTCTCAGAGGCTG 46384	232
ò	151 151	Db 45303 GTCACGCGACACAGACCTTGCAGGGAGTTAACTCCGGCCCAGGCGAGCGGCTGCGGTCA 45244
qu	46383 GTTCTGTTGGGGGAGAGCCTGGGGACTCAGGCACTGGCTTTAGCCTCATCCATGAGCGC 46324	
ò	151 151	Db 45243 TGCCTGGTGGGTCATGCTCGAAGTCACACCCAGAAGAGGCCTGGGAGGAGCTGGCCAGGG 45184
ф	46323 TAAGCCTTCCCTGCTCCCCCATCGCCCCCACCATGCTGCCTGC	
ờ		Db 45183 GCTACGACCCTCACCTCACTGCTCTGGTCAAGTGGGGCCTGGAGGGGGTCCAGGAAC 45124
dū	AGCCAGTGCAGGTCTCAGGGCCAAGCTGCGACCCTGCCCCAGGGCTCAGGAGCTCAGGTC	Qy 232 232
ò	-AspileValCys	Db 45123 TCACCTGTGCAAAAGCAGCTCCCAGGCAGGGCAGTGAGAAGCCAGGGCCCCTGCCAGGCG 45064
gg	CCGCTGCACAGTGGCTGTGCTGGGTTGAGCGGTGGCCTCTTGCAGACATAGTGTGC	Qy 232 232
à i	156 MetAspargValGluGluIleLeuGluLeuAlaAlaAlaApHisBroLeuSerArgAsp 175	Db 45063 CCCATTTCTGGGCCTCCAGCTGTGAGCTGTGCGCCTGGCCATGGCCTCTCTGAG 45004
g	ATGGACCGTGTGGAGGAGATCCTGGAGCTGCAGACCACCACTCTTTCCAGGGAC	Qy 232 232
දු ද	176 AsniyaTrpValValGlnLyaTyrlleGluThrPrOLeuLeUlleCySASDTnrLyaFne 195	Db 45003 CCCTGTTTCTCCATCTGGGACAGTAACGCTCATCCCAGCTGGGCCCCTCCAGCAGAGGGT 44944
an .	AALAAGIGGGICGGICLAGAAGIACAATCGAGACGCCGCIGCICAATCIGIGAGAACGAGGATC	ΟΥ 232 232
ð i	AsplieArgGinTrpPheLeuValThrAsplrpAshFroLeuIntleTrpPheIVILVS	Db 44943 TGGAGTCCTCAGGGGCAGGGTTCTCTAGAGCCAGCTGGGTGGG
a è	46023 GACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAG *350** 216 GluserTvrLeuArapheSerThrGlnArapheSerLeuAspLvsLeuAsp 232	Qy 232 232
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NUMBER OF SEQ ID NOS: 103
SOFWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 726
                        TYPE: DNA ORGANISM: Homo sapiens
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                                        ; NAME/KEY: CDS
; LOCATION: (1)..(726)
US-10-635-977-3
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Publication No. US20040171131A1
GENERAL IMPORATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
FILE REFERENCE: DOZBABA CIP
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: US. 60/394,725
PRIOR APPLICATION NUMBER: US. 60/394,725
PRIOR APPLICATION NUMBER: US. 10.8-10/615,659
PRIOR FILING DATE: 2002-07-09
PRIOR FILING DATE: 2003-07-09
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## APPLICANT: BATRA, Sajeev
## APPLICANT: BATRA, Liam
## APPLICANT: BATRA, Liam
## APPLICANT: POLICKY, Jean.
## APPLICANT: POLICKY, Jean.
## APPLICANT: POLICKY, Jean.
## APPLICANT: POLICKY, Jean.
## TILLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
## CURRENT APPLICATION NUMBER: US/10/27, 595A
## CURRENT APPLICATION NUMBER: US 60/201, 960
## PRIOR FILING DATE: 2000-05-08
## PRIOR FILING DATE: 2000-05-08
## PRIOR FILING DATE: 2000-06-05
## PRIOR APPLICATION NUMBER: US 60/209, 705
## PRIOR APPLICATION NUMBER: US 60/210, 149
## PRIOR APPLICATION NUMBER: US 60/210, 149
## PRIOR APPLICATION NUMBER: US 60/210, 149
## PRIOR APPLICATION NUMBER: US 60/213, 215
## NUMBER OF SEQ ID NOS: 68
## SOFTWARE: PERL PROGRAM
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; OTHER INFORMATION: Incyte ID No: 2156553CB1
US-10-275-595A-39
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              Sequence 39, Application US/10275595A
Publication No. US20040078804A1
                                                                      APPLICANT: YUB, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Dyung Aina M.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: AZIMZAI, Yalda
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YAO, Monique G.
BANDMAN, Olga
BURFORD, Neil
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ORGANISM: Homo sapiens
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us-10-635-977-2.p2n.rnpbm

411 - ArgAspleuGlyLeulysGluGluLysGlyLeulaleuleulaberoleula	34 ThrGlnGlnTyrTyrSerleuValHisGlyAsphlaPhelleSerAsnSerhzgAsnTyrDs
TITLE REFERENCE: 210121.572 FILE REFERENCE: 210121.572 CURRENT APPLICATION NUMBER: US/10/102,524 CURRENT FILING DATE: 2002-03-19 NUMBER OF SEQ ID NOS: 1863 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1765 LENGTH: 2538	1 1
; TYPE: DNA ; ORGANISM: Homo sapiens US-10-102-524-1765	н
Alignment Scores: 2.32e-95 Length: 2538 Score: 1020.00 Matches: 220 Score: Similarity: 55.5\$ Conservative: 69 Boat Total Similarity 42.2\$ Mismatches: 151	370
: 42.2% Mismatches: 35.7% Indels: 5 Gaps:	
	Db 1843
54 GInLeuvalAspileAlaCysLysvalCysGlnAlaTyrLeuGlyGInLeuGluHisGlu 73	1844
ACATG	Qy 428 OASPPrOALaGInGlyProProSerProAlaLeuGlnArgAspLeuGlyLeuLysGluGl
	Db 1900 ACAGCAAGCTGGTGGGCACTAAGGCCCTGTCGACCACAGGCAAGGCCTTGAGGACT
0.1000000000000000000000000000000000000	Qy 448 uLys

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2017 GCATCCTGAAGCCAAGAAAAGGTGGGCCTCGACCTGTGACTCACACCCAGTGGACAGTGCT 2076
                                                                                                                                            2129 ------CTGGCACCCCAAGGGAAGAGCTG 2151
                                                                                                                        2152 GICTCCCTCAGAAGCCCCTTCCTCAGAACTTCTGATCATCTCCCTCTTCTCCCCTCCT 2211
                                                   463 ------AlaGluSerGlyGlyAlaAlaGlnProThrArgThr------- 474
                                                                                 488 gHisValAspSerGlnAlaProAsnThrGlyValProValAlaGlnProAlaLysSerTr 508
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Search completed: April 4, 2006, 11:54:48 Job time: 1232 secs

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Perfect score:

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Sequence:

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Sequence 15222, A Sequence 1249, Ap Sequence 500, App Sequence 12848, A Sequence 12504, A Sequence 481, App Sequence 481, App Sequence 396, App
                                                                                                                                                                                        sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 15012, A
Sequence 173, Ap
Sequence 1, Appli
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Sequence 1091, Ap
Sequence 1245, Ap
Sequence 1245, Ap
Sequence 1254, A
Sequence 12548, A
Sequence 11822, A
Sequence 12548, A
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Sequence 12544, A
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Sequence 961, App
Sequence 15041, A
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Sequence 8
Sequence 8
                      US-09-902-540-1249
US-09-252-991A-12504
US-09-252-991A-12504
US-09-252-991A-12970
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-15041
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CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR PILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt_FL_genes Version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
18-09-620-312D-494
'S Sequence 494', Application US/09620312D
'Patent No. 6569662
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Zhao, Qing A.
Wehrman, Tom
Xue, Aldong J.
Wang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
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-MODEL=frame+_p2n.model -DEV=xlh
-O=/abss/ABSSWBE spool/US10615977/runat_04042006_103535_10086/app_query.fasta_1
-D=|abss/ABSSWBE spool/US10615977/runat_04042006_103535_10086/app_query.fasta_1
-DB=Issued_Patents_Na -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=D51ts -START=1 -END=-1 -MATRIX=b10sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-HODE=LCAL -OUTFWT=pto -NORM=ext -HBAPSIXE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02h -USFR=US10635977 @CGN 1 1 193 @runat 04042006_103535_10086
-NCPU=6 -ICPU=3 -NO_MMAP -NGG_SCORES=0 -WAIT -DSPBLCCK=100 -LONGLOG
-DEV TIMEOUT=120 -WĀRN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 138, App
Sequence 1688, Ap
Sequence 15138, A
Sequence 1651, Ap
Sequence 295, App
Sequence 56, Appl
Sequence 56, Appl
Sequence 31557, A
                                                                                                                                                      4, 2006, 09:38:21 ; Search time 288 Seconds
(without alignments)
3339.100 Million cell updates/sec
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                                                                                                                                                                                                                                                                              2854
1 MASSILKWVVSHQSCSRSSR.....LRGLKTAEGALRPPPGGKGS
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/ Cgn2 6/ptodata/1/ina/6_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/6_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/H_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/H_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PE_COMB.seq:*
/ Cgn2 6/ptodata/1/ina/PE_COMB.seq:*
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                                                                                                         OM protein - nucleic search, using frame_plus_p2n model
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US-10-104-047-1401
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US-09-799-451-295
US-09-814-915A-56
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Match Length
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Database :

305 302 271.5 228.5 210 205.5 166 154.5

Score

Result 8

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2426 TACCCACGGCTAAGGICTTCATTTCCCTCCCACGAACCTTGATTTCAAGGTGGCACCCA 2485
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acctgcgcgtgctattgaccggatgctggacgcaactgtgacacaggagcctttgag 2263
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1084 GGCGCTGACTTCGTGTTCGGGGAGGACTTCCAGCCCTGGCTGATTGAGATCAACGCCAGC 2143
                                                                           ThrileLysValAlaVal------AspArgSerCysAspIleGlyAsnPheGlu 369
                                                                                                                               LeuLeuTrpArgGlnProVal ---ValGluPro-ProProPheSerGlySerAspLeuCy 388
                                                                                                                                                                                  388 sValAlaGlyValSerValArgArgAlaArgArgGlnValLeuProValCysAsnLeuLy 408
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                                         408 sAlaSerAlaSerLeuLeuAspAlaGlnProLeuLysAlaArgGlyProSerAlaMetPr
                                                                                                                                                                                                                                                                                            428 oAspProAlaGlnGlyProProSerProAlaLeuGlnArgAspLeuGlyLeuLysGluGl
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                          ProThrMetHisProSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAsp
                                                                                                                                                         2264 CTCATCTATAAGCAGCCCGTCACCTTCCCCAGCCTCCACAAGGC------
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Jinod
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Xhao, Qing A.
APPLICANT: Xhao, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
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Ma, Yunqing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ValCysMetAspArgValGluGluIleLeuGluLeuAlaAlaABpHisProLeuSer 173
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Matches:
Conservative:
Mismatches:
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42.2$
35.7$
                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (1361)..(2419)
                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                               US-09-620-312D-494
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     SEQ ID NO 494
LENGTH: 3001
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              319 LeuGlyArgAspPheArgProTrpLeuIleGluIleAsnSerSerProThrMetHisPro 338
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                                            1715 AGGATTTGTGTGCCAAGATCCTGCCCAGGGGCATCAACTCGGCCAATTTATCCCACCTT
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                                                                             339 SerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAgpThrIle-----
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Patent No. 6942241

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT PILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PEENTLY OF SEQ ID NOS: 4096

SOFTWARE: PEENTLY OF SEQ ID NOS: 4096

SEQ ID NO 1688

LENGTH: 2624
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Mismatches:
Indels:
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AlaIleHisLeuCysAsnAsnAlaValGlnLys------TyrLeuLysAsnAsp
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APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
TILLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION WINBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_PL_genes Version 1.0
SEQ ID NO 138
LENGTH: 5314
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Matches:
Conservative:
Mismatches:
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; LOCATION: (531)..(4376)
US-09-620-312D-138
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Best Local Similarity:
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Pred. No.:
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TTTTTCGCGTTGACGAG 367
ACCTGAGGCACACCAA 1846
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                    CAGGAGCAGAACGCGGAGGACTGGAACCTGTACTG-GAGGACATCCTCTTTCCGAATGAC 486
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                                                                        CGAACA-----CAACAGTGTTAAACCGTGGCAGCAGCTAAACCACCACCCTGGAACCAC
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| CAAGCTTACCAGGAAAGACTGTTTGGCCAAACACCTGAAGCACATGAGGAGGATGTATGG
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------TyrSerLeuValHisGlyAspAlaPhelleSerAsnSer
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Sequence 15138, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

US-09-270-767-15138

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| CATCTCTGCAATTACAGCATTAACAAATACCATTCTGATTACATAAGGAGCTCCGATGCT
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Mismatches:
Indels:
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Matches:
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO 15138
LENGTH: 1980
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Best Local Similarity:
Query Match:
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	Oy 138 Db 852 GGCCTTT Oy 148 rArgGly :::: Db 912 CCAGGGC Oy 168 Db 972 GACCCGG Oy 179Val Db 1032 GCGGTG	GGCCTTTTCACCTTGATGAAACCCAGATATGGATCTGCAAGCCCACAGCCTCCAA 911 TATGGIAATGAAACCCAGATATGGATCTGCAAGCCCACAGCCTCCAA 911 TATGGIAATGAAGCTTCTTGATGAAACCCAGATATGGATCTGCAAGCCCACAGCCTCCAA 911 SINGLIAN STATGATGAAACAGAACAGAAGAAGTTGCCGCCCTGCAGGCCAA 971 CCAGGGCAAAGGCATCTTCCTGCTCCGGAACCAGGAGGAAGTTGCCGGCCCTGCAGGCCAA 971 CCAGGGCAAAGGCATCTTCCTGCTCCGGAACCAGGAGGAAGTTTCTCGGGGGCCTCAGGC 1031 GACCCGGAGCATGGAGGACGCCCATCCACCACAAGACGCCGTTCCGGGGGCCTCAGGC 1031 ValValGlnLysTyr11eGluThrProLeuLeu11eCygAspThrLysPheAsp11 197
RESULT 6 10-10-10-407-1651 Sequence 1651, Application US/10104047 Patent No. 6943241 GENERAL INFORMATION: TITLE OF INVERTION: No. 6943241e1 full length cDNA TITLE OF INVERTION: No. 6943241e1 full length cDNA TITLE OF INVERTION: No. 6943241e1 full length cDNA FILE REFERENCE: H1-A0105 FILE REFERENCE: H1-A0105 FILE REFERENCE: US/10/104,047 CURRENT APPLICATION NUMBER: US/10/104,047 PRIOR APPLICATION NUMBER: 2002-03-25 PRIOR FILING DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4096 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1651 LENGTH: 2111 TYPE: DNA CREANISM: Homo sapiens US-10-104-047-1651	Oy 197 eArgGln Db 1092 GCGCTCC Oy 217 TTyrLeu Db 1149 CTATGCT Oy 237 UCYSASN Db 1209 GACCAAC Oy 255 -LeuLeu Db 1248 GCTGCTGC Oy 274 nGlyArg	197 eArgGInTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSe
Alignment Scores: Alignment Scores: 2.66e-09	Oy 294 sAlamet Db 1317 GGCCGG Qy 314 yAlaAsp Db 1339 Qy 334 oThrMet Db 1348	294 sAlaMetLysValAlaGlnAspHisValGluProArgLysAsnSerPheGluLeuTyrGl 314
Oy 26 GlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAspAla	1375 374 1377 394 1431	
Qy 81 aValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeuVa 101 Db 741 CCTGGAGGACCTCCCGTGG	Oy 405 BABILDER Db 1491 TGGAACC Qy 420 SALAAFF ::::: Db 1551 CACCAAA Qy 440 DARGASS Db 1611 CCTCGCC Qy 456 UAlaPFC	PARILLEULYS TGGAACCAAACCTTCCAGCGTCTCTGCTCACTTAGCTGGCAGTGCCTGTCCCCAGCAGC 1550 SAlaArgGlyProSerAlaMetProAspProAlaGlnGlyProProSerProAlaLeuGl 440 :::::

----GlnAlaLeuLeuAsnArgile

312

-----TTGATTGTTCAAGAA 348

202 408 222 236 522 582 273 630 750

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Sequence 56, Application US/09814915A
Patent No. 6750015
GENEAL INFORMATION:
APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Rel
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
    80 TATGCTAGTTTGAATAGAAATTATTTTTCCTATTATGTCCAATTTACAGAAGGATCAAGT 139
                                                                                                             125 ThrSerValAsnProGlnThrAspIleAspGlyLeuArg-----AsnIleTrpileIle 142
                                                                                                                                                                            LysProAlaAlaLysSerArgGlyArgAspIleValCysMetAspArgValGluGluIle 162
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631 AATCAACATGATGTTGCTAAGTTTTGGAGAAATTGGTGGTAAAGACCCTG 690
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200 AATTCCAA-AATTATGTGAAAGAATTGAAGAAAAAGGAAAGCAGAAAACTTTTATATAGG
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                                                                                                             ---ThrGlyValProValA
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TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
                                                aAlaGlyLysValGlu-LeuProAlaCysProCysArg
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NO. 673869

LENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Tanu, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
NPELICANT: Ren, Fesyan
PLICANT: Rang, Jie
JLICANT: Zhang, Jie
JLICANT: Zhang, Jie
JLICANT: Zhang, Jia

NICANT: Wang, Jan-Rui

ANT: Chen, Rui

ANT: Yamazaki, Victoria

NT: Chen, Rui-hong

NT: Mang, Zhiwei

Wang, Dunri'

Fang, Vang,
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 295, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
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Wehrman, Tom
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ORGANISM: Homo sapiens
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Percent Similarity:
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            ----SerAlaIleHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsnAspValGl
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; Sequence 31557, Application US/09270767
; Patent No. 6703491
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CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
LENGTH: 3394
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID MOS: 62317
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31557
LENGTH: 783
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE RAPPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1522
LENGTH: 1525
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US-09-270-767-15222
US-09-270-767-15222
Sequence 15222, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                   ORGANISM: Drosophila melanogaster
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GENERAL INFORMATION:
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1249
                                                                                                                                                                                                               134 ---AspGlyLeuArgAsnIleTrpIleIleLysProAlaAlaLysScrArgGlyArgAsp
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Gaps:
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ORGANISM: Myxococcus xanthus
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153.00
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21.1%
5.4%
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31.7%
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PLING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: US 60/094,190
RICH APPLICATION NUMBER: US 60/094,190
RICH PLANTON NUMBER: US 60/094,190
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                                                                                 661 AGTGATTTCTCCGTTAATCTATTAGAAGTTAATTCATACCCT 702
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12848
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Best Local Similarity:
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                            Sequence 500, Application US/09248796A

Sequence 500, Application US/09248796A

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.13
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR PLILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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178 AACGATGAGAATGAAGAAGGAAGGAAGAGAAGAAGATAACGGTATAATTTTG 237
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58 GAAATTAATAAGAAGAAAAATTGTGGGTTTTTGAAACCTAGTATGAGTGATAAAGGTCAA 117
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Best Local Similarity:
Query Match:
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LENGTH: 780
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Qy 452 oLeuAlaLeuLeuAlaProLe Db 2712 TCAACCTGACGGGGGGGACACCGTGATCCACT Qy 468 aAlaGln	498 2889 517 2949	RESULT 14 US-09-252-991A-12504 i Sequence 12504, Application US/09252991A i Patent No. 6551795 i GENERAL INFORMATION: i APPLICANT: Marc J. Rubenfield et al. i TITLE OF INVENTION: i TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS i TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS	; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION NUMBER: 05/09/252,991A ; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788 ; PRIOR PILING DATE: 1999-02-18 ; PRIOR PILING DATE: 1999-07-27 ; NUMBER OF SEQ ID NOS: 33142	; SEQ ID NO 12504 ; LENGTH: 1212 ; TYPE: DNA ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-12504	Alignment Scores: 0.0304 Length: Pred. No.: 129.50 Matches Score: 129.50 Matches Percent Similarity: 33.9\$ Conserv Best Local Similarity: 23.4\$ Mismatch Query Match: 3 Gaps:	US-10-635-977-2 (1-541) x US-09-252-991A-12504 Qy 201 PheLeuValThrAspTrpAsnPro Db 4 TTTGCAATTACGCAATGGCGCGTTCGGATTTG	Qy 218 TyrLeuArgPheSerThrGlnArgPheSerLe	
1630 CAGCGGGGGTGCTGGCCGACGACGACGGGCTGGGCAAGACCTTGCAGTCGCTGGCCCA 1689 181 nLysTyrIleGluThrProLeuLeuIleCysAspThrLy 194 1690 CGTGCTCCTGGAAAAGCAGGCGGGGGTCGACGCGGGGGTGGTGGTGGTGCCCAC 1749 194 SPheAspIleArgGlnTrp	AGCACCTGGT hrGlnargPheSe i:: AGCGGCGGTTCCA lnLySTyrLeuLy	1930 CCTGCTGACGACGAGGGGGAACATCAAGAACGCCACCAA 1977 247 SASNASPVALGLYANGSErProLeuLeuProAlaHisAsnMetTrpThrSerThrAr 266 1978 GGCGCGCGCGCGCGGGGGGGGGGGGGGGCTGGCTGGCTG	286 oSerMetLysLysAlalleAlaHisAlaMetLysValAlaGlnAspHisValGluProAr 306	323 eArgProTrpLeulleGlulleAsnSerSerProThrMetHisProSerTh 340	ccrdcccrccadrccccadacrcccadaccccadcccad	363	CTGATCGCCGAGGSTCGCCGGGTCC LaSerLeuLeuAspAlaGlnProLe	
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cccGGCCGCCGCGGGGGCTCAAGGC 174
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                                                                                               GlnAlaPro------AsnThrGl 498
                                                                                                                                              AspProAsnGlnLeuAsnAlaHis---- 516
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PRIOR APPLICATION NUMBER: US 60/094,190	Qy 201 PheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSer 217 Db 1236 TTTGCAATTACGCAATGGCGCGTTCGGATTTGCCGAACGCCATGGAGT 1189 Qy 218 TyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAspSerAlaileHisLeu 237 Db 1188 GCCATGCATTCGATCTGCCGACCTGGCTTCATCGA 1147 Qy 238 CysAsnAsnAlaValGlnLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuPro 257 Ph 1116	258 AlaHisAsmMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGly 1098	Db 932 CTGAAGAGCGAGTTCACCGAGCGAC—-GCCGCGGGCATATCCGCATCTT 892 Oy 322	374 Inproval-valdlupro
Oy 286 -ProSerMetLysLyshlallehlaHishlaMetLysValAlaGlnAspHisValGlubr 305	Inproval-valglupro	423 GlyLeuProLeuAlaberDroAlaGlnGlyProProSer		Db 982GGGCTCCGGAGAATCGGCGGACAACCGCCAGGCGGT 1017 RESULT 15 US-09-252-991A-12970/c ; Sequence 12970, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; CURRENT APPLICATION NUMBER: US/09/252,991A ; CURRENT FILING DATE: 1999-02-18 ; PRIOR FILING DATE: 1998-02-18

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585 CACCCTGCACGCCTTCCTGTACGAACGGGTGGAGCAGATGGGCGAGCAGCTATCGCTGCG 526	ProAlaLeuGlnArgAspLeuGlyLeuLysGluGluLys 449	525 CATCCAGGTCTCCAGCTTCGAGGCGATCTGCCGGATGATCGAGGGCGGCGTCGGCATCGG 466	450 GlyLeuProLeuAlaLeuLeuAlaProLeuArgGlyAlaAlaGluSerGlyGly 467	465 CGTGATCCCCCAGTCCGCCGCCGCCCCACAGCCGGACGATGAAGCTGGCGACCATCGA 406		405 ACTCGACGAGCCCTGGGGGATCCGCGGGGCGCCTGCTGGTACGCGACCTGGAAGCACT 346	480 ValGluLeuProAlaCysProCysArgHisValAspSerGlnAlaProAsnThrGlyVal 499	345 GCCGAGTTGCCTGCGGGCGTTGATCGAGGAGTTGCAGGGTGGG 301	500 ProValAlaGlnProAlaLysSerTrpAspProAsnGlnLeuAsnAlaHisProLeuGlu 519	AGACAGCCTGTAGGGCGGATAACGCCCCTGGCGTTGTCCGCG	520 ProValLeuArgGlyLeuLysThrAlaGluGlyAlaLeuArgProProFroGlyGly 53:	GGGCTCCGGAGAATCGGCGGACAACCGCCAGGCGGT 22:	
S CACCCT	437Pro	S CATCCA	so GlyLeu	SS CGTGAT	468	S ACTCGA	30 ValGlu	IS GCCGAG	0 Proval	300	20 Proval	258	
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Search completed: April 4, 2006, 09:44:02 Job time: 333 secs

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AY415398 12-DEC-2003
Homo sapiens HCM5544 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
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1 (bases 1 to 1259)

ClarkA.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A..

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.
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Science 302 (5652), 1960-1963 (2003)
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AUTHORS
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REFERENCE
AUTHORS
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AY415398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
    -MODELE frame+ p2n.model - DEV=x1h
-Q=/abss/ABSSWEB spool/US10635977/runat_04042006_103532_10020/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10635977/runat_04042006_103532_10020/app_query.fasta_1
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-LOOPCR1=0
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits - START=1 - END=-1 - MATRIX=100 - THR MIN=0 - ALIGN=15 - MODE=LOCAL
-OOTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=2000000000 - HOST=abss07
-NOTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=2000000000 - HOST=abss07
-NO MMAP - NEG SCÖRES=0 - WAIT - DSPBLOCK=100 - LONGLOG - DEV TIMEOUT=120
-WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPEXT=7
-YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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AY415399 Pan trog1
AK030151 Mus muscu
AK029745 Mus muscu
                                                                                                                                     4, 2006, 09:35:51 ; Search time 5994 Seconds (without alignments) 4222.858 Million.cell updates/sec
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                                                                                                                                                                                                                                           2854
1 MASSILKWVVSHQSCSRSSR......LRGLKTAEGALRPPGGKGS 541
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                   GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                               OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                              41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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7.0
7.0
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Kgapop 10.0 , Kgapext
Ygapop 10.0 , Ygapext
Kgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length
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TITLE JOURNAL

COMMENT

AY415400 Mus muscu CR745100 CR745100 AK080321 Mus muscu

AY415399 AK030151 AK029745 AY415400 CR745100 AK080321

1259 1257 2969 2720 1265 770 2520

2129.5 1963.5 1755 1732.5 1639 1639 1052

Score

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Database :

4 10 7 4

61.5 60.7 57.4 47.7 36.9

AY415398

W31827 zb94f04.rl BQ327883 MR4-RT004 BP305902 BP305902

DQ04586 HOMO SAPINE BMB008517 AGENCOURT DQ045869 PAIN LTOGI CK597795 AGENCOURT CK597795 AGENCOURT CK597795 CJ018705 CX95696 JGI CAAO8 CX95686 JGI CAAO8 CX956867 JGI CAAO8 BC028169 HOMO SAPINE BM717061 UL -E-GJ0-CK966757 CR96615 DN831611 MGCI.7.1. CC89661 CR998661 DN722875 CN832-GO5 CK653583 AGENCOURT CK653583 AGENCOURT CK64006 AGENCOURT CK64006 AGENCOURT CK64006 AGENCOURT CK64039072 AGENCOURT CK64039 AGENCOURT CK64039 AGENCOURT CK64039 AGENCOURT CK64039 AGENCOURT CK64039 AGENCOURT CK64039 AGENCOURT CK6404243 170006000 BW740389 BW740389 CF999072 AGENCOURT CK646623 AGENCOURT CR9446623 AGENCOURT CK646623 CR746623 CR74644665 CR74644665 CR74644665 CR74644665 CR74644665 CR74644665 CR74464665 CR7444665 CR7446465 CR7446466 CR7444676 CR74446465 CR7446466 CR7444665 CR7446466 CR7444646
	321 ArgaspheargProTrpLeulleGlulleAsnSerSerProThrMetHisProSerThr 321 ArgaspheargProTrpLeulleGlulleAsnSerSerProThrMetHisProSerThr 321 ArgaspheargProTrpLeulleGlulleAsnSerSerProThrMetHisProSerThr 321 ProvalThralaGluLeuCysAlaGluValGluGluAspThrIleLysValAlaValAsp	1058 CCGGTCACGCCCACCTGTGTGCACGGTGCACGGAGGAGGACCTTCAGGTGGCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	Oy 381 ProPheSerGiySerAspleuCysValAladiyValSerValArgArgArgGun 400	1198	1198	441 ArgAsphenGiybenLybstucinDyssiybenFlobenArgabenDariobenArg 1198	1198	481 Glui 1199C	Qy 501 Val 501 Db 1256 GTA 1258	RESULT 2 AY415399 AY415399 LOCUS AY415399 DEFINITION PAN LYGGLOGYCES HOME TRANSCRIPT, partial sequence,	GENORIC BUIVEY SEQUENCE. ACCESSION AY415399.1 GI:39771358 KEYWORDS GSS.	NISM	REFERENCE 1 (bases 1 to 1257) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.	Adams, M.D. and Cargill, M. Title Mann-Chimpenone orthologous gene trios Science 302 (5652), 1960-1963 (2003)
them based on alignment. Location/Qualifiers 1. 1259 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="kaxon:9606" <1 >1259 /locus_tag="HCM5544"	Alignment Scores: 3.46e-175 Length: 1259 Pred. No.: 2129.50 Matches: 413 Score: 2129.50 Matches: 413 Percent Similarity: 82.4% Mismatches: 1 Query Match: 10 Gaps: 1 Gaps: 1	977-2 (1-541) x AY415398 (1-1259) 1 MetAlaSerSerIleLeuLyGTrDValValSerHisGlnSerCysSerArgSerSerArg 20	ъ В	41 AlaGluAsnAlaGluAlaLysLeuArgGlyLeuProGlyGlnLeuValAspIleAlaCys 60 	61 LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAsp 80 		101 ValHisGlyAspAlaPheIleSerAsnSerArgAsnTyrPheSerGlnCysGlnAlaLeu 120 	121 LeuAsnArglleThrServalAsnÈroGlnThrAsplleAspGlyLeuArgAsn1leTrp 140 		GluileLeuGluLeuAlaAlaAlaAspHisProLeuSerArgAspAsnLysTrpValVal 	181 GINLYSTYTIIGGIUTHrProLeuLeuIIeCYSASPTHrLYSPHeASPIIeArgGINTrp 200 	201 PheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrIysGluSerTyrLeuArg 220 	221 PheSerThrGlnArgPheSerLeuAspLysLeuAspSerAlaileHisLeuCysAsnAsn 240 	241 AlaValGinLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsn 260

221 PheserThrGlnhrgPheserLeuAspLysLeuAspSerAlaileHisLeuCysAsnAsn [Oy 301 AsphieValGluProArgLysAssnSerPheGluLeuTyrGlyAlaAspPheValLeuGly 320 1	Qy 361 ArgSerCysAspIleGlyAsnPheGluLeuLeuTrpArgGlnProvalValGluProPro 380	Qy 401 ValLeuProValCysAsnLeuLysAlaSerAlaSerLeuLeuAspAlaGlnProLeuLys 420 Db 1198 Qy 421 AlaArgGlyProSerAlaMetProAspProAlaGlnGlyProProSerProAlaLeuGln 440 Db 1198	441 ArgAspLeuGlyLeuLysGluGluLysGlyLeuProLeuAlaLeuLeuAlaProLeuArg 1198	481 GluLeuProAlaCysProCysArgHisValAspSerGlnAlaProAsnThrGlyValPro 	DEFINITION Wis musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933401817 product:hypothetical Tubulin-tyrosine ligase containing protein, full insert sequence. ACCESSION AK030151. G1:26326134 VERSION AK030151.1 G1:26326134 KEYWORDS HTC; CAP trapper. SOURCE Mus musculus (house mouse) NGGANISM Mus musculus (house mouse) SOURCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;	REFERENCE 1 AUTHORS Carninci, P. and Hayashizaki, Y. TITLE High-efficiency full-length cDNA cloning
REFERENCE 2 (bases 1 to 1257) AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE Direct Submission Colera Genomics, 45 West Gude Drive, Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FEATURES Location/Qualifiers Source // Coganism="Pan troglodytes" // Mol type="genomic DNA" // Mol type="	ORIGIN Alignment Scores: Pred. No.: Pred. No.: Score: Score: 1.11e-160 Length: 1257 Score: 1963.50 Matches: 386 Percent Similarity: 77.6% Conservative: 25 Guery Match: 68.8% Indels: 88 DB: US-10-635-977-2 (1-541) x AY415399 (1-1257)	MetalaSerSerIleLeuLy9TrpValValSerHisGlnSerCysSerArgSerSerArg	/8 41 138 61	198 AAGGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGACATCGACACGTCAGCAGAT 81 AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu	Db 318 GTTCANNNNATGCTTTCATCTCCAATTCAAGAAATTACTTTTCGNANNNCCAGGCTCTG 377 Qy 121 LeudsnArglleThrSerValAsnProGlnThrAspIleAspGlyLeuArgAsnIleTrp 140	438 ATTATAAAGCCGGGCCAAGTCCCGGGGCCGAGACATGTGTGTG	<pre>Qy 201 PheleuvariThrAppTrpAenProLeuThrIleTrpPheTryUpsGluseTryCendigs 220 </pre>

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RQLTEKA KERKIFSI VGHYPVIRATIERKGWVEKKFNFFPRALQMIGSBDKGARTKE

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RQSIALERFDDIHDVMSRIUWRDIPPRPRCYGCTEBERQBELDDFRRTYAASILEKWVILAD

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PKVRSARALMETVIRPPRYGSSKVPGVTLTSAQHPRALFAQTMKRTQWTSSPPPTASGNH

RDSSPFCPIVFEELWLAPRORRPSSCILQSRAGMIRGIP"
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                  'note="unnamed protein product; hypothetical
                                          Tubulin-tyrosine ligase containing protein (InterPro|IPR004344, evidence: InterPro)
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Query Match:
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/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Of 10,70 full-length cDNAs
(Asture 420, 565-573 (2002)
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Location/Qualifiers
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/db_xref="FANTOM_DB:4933401B17"
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F., Imotani, K., Ishii, Y., Itoh, M., Komo, H., Kawa, T.,
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ulus adult male testis cDMs, RIKEN full-length enriched clone:4930524KG7 product:hypothetical Tubulin-tyrosine containing protein, full insert sequence.
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      Experimental Animal Research in Riken contributed
                                                                                                                                                                                                                         /note="unnamed protein product; hypothetical
Tubulin-tyrosine ligase containing protein
(InterPro|IPR004344, evidence: InterPro)
                                                                                                                                                                           /tissue_type="testis"
/clone_lib="RIKEN full-length enriched
/dev_stage="adult"
334. .2490
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337
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                                further details
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="PANTOM_DB:4930524K07"
/db_xref="raxon:10090"
/clone="4930524K07"
/sex="male"
                    prepare mouse tissues.
Please visit our web site for furth
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
IR.:http://fantom.gsc.riken.jp/.
ORL:http://fantom.gsc.riken.jp/.
Organism="Mus musculus"
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
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                                            LeuLeuAsnArgIleThrSerValAsnProGlnThrAspIleAspGlyLeuArgAsnIle
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
1 (bases 1 to 1265)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferricra, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                         15400 1265 bp DNA linear GSS 12-DEC-2
musculus HCM5544 gene, VIRTUAL TRANSCRIPT, partial sequence,
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus tag="HCM5544"
                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                   genomic survey sequence.
AY415400
AY415400.1 GI:39771359
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Pred. No.:
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AKO80321

Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630053H17 product:HOTTL PROTEIN homolog [Homo sapiens], full insert sequence.
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303 GAGACGCCGCTGCTCATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACG 362
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                 ArgPheSerLeuAspLysLeuAspSerAlalleHisLeuCysAsnAsnAlaValGlnLys
                                                                                                                                                                                     TyrleuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsnMetTrpThrSer
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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/lab host="DHIDB"
/clone lib="Soares testis_NHT"
/clone lib="Soares testis_NHT"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
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 Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
Peters,M., Radelof,U. and Schneider,D.
I.M.A.G.E. cDNA Clone Collection
Unpublished (2004)
                                                                           Contact: Inge Arlart

Par D Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD.INAGp998M164174.
RZPDLIS: I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg G, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information.
Ml3r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGp998M164174 ; IMAGE:1645239"
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LMTLPTAKVLMSFPPHDLKLAPSMLKPGKVGFELCCTTWRVYLSGGIGEEGHRQRAA
PRPSSAPGKGLSSTEPCSKTET"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Adenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Jease vist our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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/tissue type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev grage="3 days neonate"
84. 7.2198
                                           Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C5TBL/G3"
/db_xref="FANTOM DB:A630053H17"
/db_xref="taxon:I0090"
                                                                                                        Nature 420, 563-573 (2002)
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              Length:
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1.37e-80
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	Db 3789 GTCTCCCTCAGAAGCCCCTTCCTCCACAGA	3849	Qy 538 y 538 Db 3897 A 3897		BU937372 LOCUS BU937372 DEFINITION AGENCOURT_10519180 NIH_MGC_169 N	IMAGE: 6705256 5', mRNA sequence ACCESSION BU937372. VERSION BU937372.1 GI:24126191 KEYWORDS EST.		Mammalla; Eutheria; Euarchontogl Sciurognathi; Muroidea; Muridae; REFERENCE 1 (bases 1 to 775) AITHORS NIH-MSC Phthal/Amed nei nih Amed		COMMENT Contact: Robert Strausberg, Ph.D Email: cgapbe-remail.nih.gov. Tissue Procurement: Dr. Jonathan	CDNA Library Preparation: Mich CDNA Library Arrayed by: The I DNA Sequencing by: Agencourt E Clone distribution: MGC clone	found through the I.M.A.G.E. Con http://image.llnl.gov	Plate: LLCM3002 row: g column: High quality sequence stop: 569.	rce	/ "Lo _ roype=" muses 10090"	/lab_host="Dh108 (T1-ph	(ggccattatggc); Site 2 (ggccattatggc); Site 2 by olig-dT priming and	5 - AGCAGTGGTATCACGCGG 5 - ATTCTAGAGGCCGGAGGCGGC	enriched library was co Creator SMART kit and s	BIZE fraction. Library Brownstein (NIMH, NIH)		ent Similarity: 83.6%	DEST LOCAL SIMILATITY: /3.8* MASSMA (Query Match: 5 Gaps: DB:	US-10-635-977-2 (1-541) x BU937372 (1-775)	Qy 197 IleArgGlnTrpPheLeuValThrAspTrp	
174 ArgAspAsnLysTrpValValQlnLysTyrileGluThrProLeuLeulleCysAspThr 193	2832 AAGGACGGCAAGTGGGGGCCCAAGTATATTGAGCGGCCCCTCCTCATCTTTGGCACC 2891	194 LysPheAspIleArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPhe 213	TyrLysGluSerTyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAspSer		234 AlaileHisLeuCysAsnAsnAlaValGinLysTyrLeuLysAsnAspValGlyArgSer 253 :::::: ::::: ::: 3012 TCAGTGCACCTGTGCAACAACTCCATCCAGAAGCACCTGGAGAACTCATGGCATCGGGAT 3071	254 ProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArg 273	274 GlnGlyArgGlyAlaValTrpGlySerVallleTyrProSerMetLysLysAlaileAla 293	HisAlaMetLysValAl	CACGCACTTCAGACCTCCCAGGACACCGTGCAGTCGGAAGGCCCAGCTTTGAGCTCTAT	314 diyalaapphevalleudiyargaappheArgproTricelliedilalasserser 333 	334 ProthrMetHisProSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAsp 353		3372 ACCTGGGGTGGTCATTGACGGGATGCTGGACCGCAACTGTGACAGGGGCCTTTGAG 3431	370 LeuLeuTrpArgGlnProValValGluPro-ProProPheSerGlySerAspLeuCy 388	sValAlaGlyValSerValArgArgAlaArgArgGlnValLeuProValCysAsnLeuLy	3480 3480	408 sAlaSerLalaSerLeuLeuAspAlaGlnProLeuLysAlaArgGlyProSerAlaMetPr 428			urysGlyLeuProLeuAlaLeuLeuAlaProLeuArgGlyAla	3594 TACCCACGCCTAAGGTCTTCATTTCCCTCCCACGAACCTTGATTTCAAGGTGGCACCCA 3653 463AlaGluSerGlyGlyAlaAlaGlnProThrArgThr 474	CAGTGGACAGTGCT				
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cles, Vector: pDNR-LIB; Site 1: Sfil te_2: Sfil (ggcgctctggcc); cDNA made and directionally cloned. 5' and 3' in cloning as follows: GCAGAGTGGCCATTACGGCGGG-3' and CGGCCGACATG-dT(30)NN-3'. Full-length s constructed using the Clontech and size-selected to contain the 0.5 kb ary created in thelaboratory of M. IH). Note: this is a NIH_MGC Library."
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) Mus musculus cDNA clone
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                         GACTICIGATCATCTCCCTTCTCCCCTCCT 3848
                                                                  LeuArgPro------ProProGlyGl 538
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Bioscience Corporation
distribution information can be
consortium/LLNL at:
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294 HisAlaMetLysValAlaGlnAspHisValGluProArgLysAsnSerPheGluLeuTyr 313
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Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
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/gene="ARPC4"
/locus_tag="HC11626"
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
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1 (bases 1 to 1059)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sack
Nielsen, R., Bustamante, C., Tanenbaum, D.M., Civello, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Huchimpanzees
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         107 IleSerAsnSerArgAsnTyrPheSerGln------CysGlnAlaLeuLeuAsnArg 123
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                                      14 GTCCGCGGGACGAGGCACCTCTACACTCCAGGTCCAGCGCTGTGAGGACATCCTGCAGCAG
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//clone_logan: brain, Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: Not1; RNA Source male hippocampus, age 27. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear EST 05-MAR-2002
sapiens cDNA clone IMAGE:5734232
                                                                                                                                                            Hominidae; Homo.

E 1 (bases 1 to 1023)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabe-remail.nih.gov

Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM12739 row: d column: 09

High quality sequence start: 6

High quality sequence start: 6

High quality sequence stop: 664.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Matches:
Conservative:
Mismatches:
Indels:
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/tissue_type="hippocampus"
/lab_host="DH10B"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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אטטב-טטט 1059 bp DNA linear GSS 02-JUN-2005
Pan troglodytes ARPC4 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
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1 (bases 1 to 1059)

Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

A Scan for Positively Selected Genes in the Genomes of Humans and
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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GluserTyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAspSerAlalle
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                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC Clone distribution information
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: Library row: a column: 09
High quality sequence start: 78
High quality sequence stop: 658.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
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Site_2: Not1; RNA obtained from testis tissue of 8 wk old animal. Tissues were snape-frozen and kept at -80c before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5-pGACTAGGTTCAGATCGCGAGCGCCCC(T) 25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 1.9 kb. This primary library is normalized (non-normalized primary library is normalized (non-normalized primary library is NIH MGC_237) and was constructed by Express Genomics
(FrederIck, MD)"
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ESSI.

Rattus norvegicus

Sciurognathi; Muroidea; Murinae; Rattus.

Sciurognathi; Muroidea; Murinae; Rattus.

Sciurognathi; Muroidea; Murinae; Rattus.

Rattus.

Sciurognathi; Muroidea; Murinae; Rattus.

Rattonal Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Office of Cancer Genomics

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

ONA Library Preparation: Express Genomics

CONA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Contact: LaAMISCA row, o column: 05

High quality sequence stop: 693.

Location/Qualifiers

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                                                         Email: Muenishioaffic.go.jp

EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
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44
44
    Sciences
National Institute of Agrobiological Sciences
2 Ikenodai, Teukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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Okunishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamasima, N. and Awata, T.

PEDE (Pig EST Data Explorer): construction of a database for ESTs
effectived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
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Animal Genome Laboratory, Genome Research Department
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BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocribe-Gen; antinflammatory; anabolic; hypertensive;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; cesticular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
parkinson's disease; immunological disorder; arthritis; asthma; AIDS;
  Adj93361 Human BGS
Adq17814 Human sof
Adj93359 Human BGS
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Adj93362 Human BGS
Adj93363 Human BGS
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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ADJ93364
ADJ93362
ADJ93363
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Database :

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disorders, testicular disorders, testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, colon cancer, stomach cancer, colon cancer, stomach cancer, of the testis, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polynucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's disease to scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of a cDNA which encodes the human BGS-42 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel testis-specific tubulin tyrosine-ligase -like polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory
                                                                                                                                                                                                                                                                                                                                                                                                           e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antiabcterial, immunosuppressive, antiaeborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be useful for gene therapy. The BGS-42 polypeptide or polynucleotide can be used for disgnosing a pathological condition or a susceptibility to a pathological condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin-carboxypeptidase activity, aberrant cellular proliferation, reproductive
                                                                                                                                                                                                                                                                                                                                                                                    New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
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Matches:
Conservative:
Mismatches:
Indels:
                                      protein"
                                    /product= "Human BGS-42
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                                                                                                                                                               09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                                                                                                      Nelson TC;
153. .1778
/*tag= a
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P-PSDB; ADJ93358.
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Best Local Similarity:
Query Match:
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                                                                                WO2004005487-A2
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CDS
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MetAlaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArg

Gaps:

(1-1838)

x ADJ93357

US-10-635-977-2 (1-541)

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21 213

SerLysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAsp 40

1052 1172 1232 340 400 401 ValLeuProValCysAsnLeuLysAlaSerAlaSerLeuLeuAspAlaGlnProLeuLys 420 GlySerValileTyrProSerMetLysLysAlaIleAlaHisAlaMetLysValAlaGln 300 140 180 200 752 220 240 872 992 100 452 120 392 332 ProPheSerGlySerAspLeuCysValAlaGlyValSerValArgArgAlaArgArgGln caitcagcggarccaacctcracgraacagacarcaarataagagaacaagacaa AspHisValGluProArgLysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGly AGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCATGCACCCGTCCACG ProvalThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIleLysValAlaValAsp cedercaceccaderrerrerrecacaderacadadadacacearcaaderegecerredade ArgSerCysAsplleGlyAsnPheGluLeuLeuTrpArgGlnProValValGluProPro 273 GCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGACATCGCGTGC | IleIleLysProAlaAlaAlaSerArgGlyArgAspIleValCysMetAspArgValGlu GlulleLeuGluLeuAlaAlaAlaAspHisProLeuSerArgAspAsnLysTrpValVal GAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACAACAAGTGGTGTTT PheleuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSerTyrLeuArg PheSerThrGlnArgPheSerLeuAspLysLeuAspSerAlaIleHisLeuCysAsnAsn gecerceagaagracercaagaargargreegeceecageceecreergeeceecacacaa MetTrpThrSerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGlyAlaValTrp ArgAspPheArgProTrpLeuIleGluIleAsnSerSerProThrMetHisProSerThr LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspIlhrSerAlaAsp aagengreccageccraccrogegcagcregagcargaggacarccarcarcarcagadar ValHisGlyAspAlaPhelleSerAsnSerArgAsnTyrPheSerGlnCysGlnAlaLeu GTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATTACTTTTCGCAGTGCCAGGCTCTG LeuAsnArgileThrSerValAsnProGlnThrAspIleAspGlyLeuArgAsnIleTrp GlnLysTyrIleGluThrProLeuLeuIleCysAspThrLysPheAspIleArgGlnTrp Trecretatacaacretaaaceeeraacareraarieracaadaagarratracag AlaValGlnLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsn AlaGluAsnAlaGluAlaLysLeuArgGlyLeuProGlyGlnLeuValAspIleAlaCys 341 1053 1113 1173 1233 1293 141 873 933 281 993 301 321 361 381 61 333 101 453 121 513 573 161 633 181 693 201 753 221 813 241 261 g g g 용 ð g 용 ò a g 셤 ò g ò 임 ઠે 8 ò 8 ò Š à 셤 ద ò 셤 ò 8 g ò ò g 8 ò

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BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
anti-Miv, endocribe-Gen; antinartharitic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiartharitic; antiasthmatic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
small intestine; brain; lymph tissue; infertility; Cushing;
emphysema; pneumonia; Addison's disease; acromegaly; Alzhaimer's disease;
parkinson's disease; immunological disorder; arthritis; asthma; AIDS;
                                                           ArgAspLeuGlyLeuLysGluGluLysGlyLeuProLeuAlaLeuLeuAlaProLeuArg
                                                                                                                                                   GAGCTCCCGGCCTGTCCCCTGTCGCCACGTGGACAGTCAGGCCCCCAAACACCGGTGTCCCC
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                                 GCACGGGCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCCATCACCAGCTCTCCAG
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 AlaArgGlyProSerAlaMetProAspProAlaGlnGlyProProSerProAlaLeuGln
                                                                                                                               GlyAlaAlaGluSerGlyGlyAlaAlaGlnProThrArgThrLySAlaAlaGlyLySVal
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/product= "Human tubulin tyrosine ligase protein"
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This invention relates to a novel testis-specific tubulin tyrosine-ligase—
like polypeptide, designated the BGS-42 polypeptide. The invention may
completed for the development of compounds with a cytostatic, respiratory
completed for gene the development of compounds with a cytostatic, respiratory
completed for gene the development of completed for antipacterial,
antiinflaumatory, anabolic, hypertensive, osteopathic, nootropic,
antiinflaumatory, anabolic, hypertensive, osteopathic, nootropic,
antiinflaumatory, antiseborrheic or dermatological activity acting as
tyrosine ligase modulators. In addition, the disclosed sequences may be
useful for gene therapy. The BGS-42 polypeptide or polynuclectide can be
useful for gene therapy. The BGS-42 polypeptide or polynuclectide can be
useful for gene therapy. The BGS-42 polypeptide or polynuclectide can be
useful for gene therapy. The BGS-42 polypeptide or polynuclectide can be
completed in subject, and for preventing, treating or
ameliorating a medical condition, such as a disorder related to aberrant
completed activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, brain cancer, liver cancer, pulmonary disorders,
completed including armall intestine, brain or lymph tissue. The BGS-42
polypeptide can be used as a preventive agent for immunological
disorders including arthritis, asthma, AIDS, sepsie, acre, signers and
completed including arthritis asthma, AIDS, sepsie, acre, signers and
completed including arthritis asthma, AIDS, sepsie, acre, signers and
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completed including arthritis asthma, AIDS, sepsie, acre, signers and
completed including arthritis asthma, appeared to purify of the
cubular tyroshin ligase 
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                                                                                                                                                                       or preventing, treating or ameliorating a medical condition, ecellular proliferation, reproductive disorders or testicular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 SerlysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerArgGlnAsp
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                                                                                                                                              New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or amellorating a medical condition, aberrant cellular proliferation, reproductive disorders or testicular
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Indels:
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Matches:
                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 12; 343pp; English.
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2843.00
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                         Nelson TC;
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                         Wu S,
                                                                                               P-PSDB; ADJ93365
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AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu

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This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antiinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiathmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
demaclojodical; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
brain cancer; liver cancer; colon cancer; secmach cancer; neural disorder;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
emphysema; sethma; AlDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular
GGGGCAGCCGAGAGCGGTGGAGCCGCCACCGCCACCGCACCAAGCTG
                                                                                                              GAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCCAAACACGGGTGTCCCC
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                                                                                                                                                              ValAlaGlnProAlaLysSerTrpAspProAsnGlnLeuAsnAlaHisProLeuGluPro
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                                                                     GluLeuProAlaCysProCysArgHisValAspSerGl
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immunosuppressive, antiseborrheic or dermatological activity acting as useful for gene therapy. The BGS-42 polypeptide or polymotheotide can be useful for gene therapy. The BGS-42 polypeptide or polymotheotide can be useful for gene therapy. The BGS-42 polypeptide or polymotheotide can be used for diagnosing a pathological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin ligase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, stomach cancer, lung cancer, gastrointestinal disorders, colon cancer, stomach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymotheotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, AIDS, sepsis, acne, Sjogren's classae the BGS-42 polypeptides. The present sequence is that of a DNA traget the BGS-42 polypeptides. The present sequence is that of a DNA traget. 888888888888888888888888888888888

Sequence 1859 BP; 418 A; 563 C; 562 G; 316 T; 0 U; 0 Other;

1859	522 0	4	17	7	
Length:	Matches: Conservative:	Mismatches:	Indels:	Gaps:	(1-1859)
1.81e-166	2698.50 96.5%	96.5%	94.6%	12	x ADJ93362
Alignment Scores: Pred. No.:	Score: Percent Similarity:	Best Local Similarity:	Query Match:	DB:	US-10-635-977-2 (1-541) x ADJ93362 (1-1859)

559-0T-S0	1 / 6 -	US-IU-635-9//-Z (I-541) X ADU9336Z (I-1859)
δ	7	MetAlaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArg 20
qq	47	47 ATGGCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGGAGA 106
ò	21	
qq	107	AGCAAGCCCAGGGACCAGAGGGGGGGGGGGGGGGGGGG
ò	41	
q	167	GCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGGACATCGCGTGC 226
à	61	LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAsp 80
q	227	AAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATGGACACGTCAGCAGAT 286
š	81	AlaValGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu 100
q	287	GCCGTGGAGGACCTCACTGAGGCCGAGTGGAGACCTGACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
ò	101	ValHisGlyAspAlaPheIleSerAsnSerArgAsnTyrPheSerGlnCysGlnAlaLeu 120
QQ	347	
ò	121	LeuAsnArglleThrSerValAsnProGlnThrAspIleAspGlyLeuArgAsnIleTrp 140
g	364	CTGAATAGAATCACGTCTGTGAACCCTCAGACGGACATTGACGGGCTCCGGAACATCTGG 423
à	141	llelleLysProAlaAlaLysSerArgGlyArgAspIleValCysMetAspArgValGlu 160
QQ	424	ATTATAAAGCCCGCGGCCCAAGTCCCCGGGCCGAGACATAGTGTGTGT
λά	161	GluIleLeuGluLeuAlaAlaAspHisProLeuSerArgAspAsnLysTrpValVal 180
qo	484	GAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACAACAAGTGGGTGG
λ	181	
qc	544	CAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACATCCAAGTTCGACATCAGACAGTGG 603

||| 1620 TCA 1622

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RESULT

ò	201	PheLeuValThrAspTrpAsnProLeuThr1leTrpPheTyrLysGluSerTyrLeuArg 220
QQ	604	TTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGG 663
ò	221	PheSerThrGlnArgPheSerLeuAspLysLeuAspSerAlalleHisLeuCysAsnAsn 240
qa	664	TICTCAACTCAGCGCTICTCCCTGGACAGCTGGACAGCGCCCATCCACCTGTGCAACAAC 723
ð i	241	241 AlaValGlnLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsn 260
g (724	GCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCAGCCCCCTGCTGCCCGCACACAC 783
දු දු	261	MetTrpThrSerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGlyAlaValTrp 280 - - - - - - - - -
ò	281	GlySerValIleTyrProSerMetLysLysAlaIleAlaHisAlaMetLysValAlaGln 300
qq	844	
ò	301	AspHisValGluProArgLysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGly 320
Ор	904	GACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGGCTGACTTCGTCCTTGGG 963
ζ	321	ArgAspPheArgProTrpLeuIleGluIleAsnSerSerProThrMetHisProSerThr 340
qq	964	AGGACTTCAGGCCCTGGCTGATCGAGTTCAGCCCCACCATGCACCCCGCCACCATGCACC
ò	341	ProValThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIleLysValAlaValAsp 360
qq	1024	CCGGTCACGGCCCAGCTGTGTGTGTGTGTGTGTGTGTGTG
ò	361	ArgSerCysAspIleGlyAsnPheGluLeuLeuTrpArgGlnProValValGluProPro 380
QQ	1084	CGCAGCTGTGACTTCGAGCTCCTGTGGAGCCGGTGGTTGAGCCGCCC 1139
ò	381	ProPheSerGlySerAspLeuCysValAlaGlyValSerValArgArgAlaArgGln 400
ДQ	1140	CCATTCAGCGGGTCCGACCTCTGCGTGGCGGTCAGTGTGTGT
ò	401	ValLeuProValCysAsnLeuLysAlaSerAlaSerLeuLeuAspAlaGlnProLeuLys 420
qq	1200	GTGCTGCCCGTCTGCAACCTCAAGGCCTCGCTTCGCTGTTGGACGCGCAGCCGCTGAAG 1259
ò	421	AlaargGlyProSerAlaMetProAspProAlaGlnGlyProProSerProAlaLeuGln 440
DP	1260	GCACGGGGCCCTCGGCCATGCCAGGCCCCAGGGACCCCCATCACCACCACCCCCATGCTCTCCAG 1319
ò	441	ArgAspLeuGlyLeuLysGluGluLysGlyLeuProLeuAlaLeuLeuAlaProLeuArg 460
QQ	1320	CGGGACTTGGGACTGAAGGAAGAAGGGGCTCCCCCTGGCCTTGCTGCCTTAAGG 1379
δ	461	GlyalaAlaGiuSerGlyGlyAlaAlaGlnProThrArgThrLysAlaAlaGlyLysVal 480
Op	1380	GGGCCAGCCGAGGCGCGCCGCCCACCGGCCCAAAGCTGCTGGAAAGTG 1439
ò	481 (GluLeuProAlaCysFroCysArgHisValAspSerGlnAlaProAsnThrGlyValPro 500
ф	1440 (GAGCTCCCGGCCTGCCCTGTCGCCGCGGGGCGCCCCAACACCCGGTGTCCCCC 1499
ò	501	ValAlaGinProAlaLysSerTrpAspProAsnGinLeuAsnAlaHisProLeuGluPro 520
DP	1500	GTAGCCCAGCCCGCCAAAAGCTGGGTTCCAAACCAGCTAAATGAGCACCCGCTGGAGCCT 1559
à	521	
QQ	1560 (STECTGCCGAAGCCTGAAGACAGCAGAGGCGCGCTGCGTCCGCCGCGGAGGAAAAGGT 1619
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This invention relates to a novel testis-specific tubulin tyrosine-ligase
-like polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
-gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen,
-den, gastrointestinal-Gen, neuroprotective, notropic,
-dentiparkinsonian, antiathritic, antiasthmatic, antihar, acting as
-tyrosine ligase modulators. In addition, the disclosed sequences may be
-cused for diagnosing a pathological condition, the disclosed sequences may be
-cused for diagnosing a pathological condition, such as a disorder related to aberrant
-cubulin ligase activity, aberrant cellular proliferation, reproductive
-cutoulin ligase activity, aberrant cellular proliferation, reproductive
-cutoulin ligase activity, aberrant cellular proliferation, reproductive
-carboxypeptidase activity, aberrant cellular proliferation, reproductive
-carboxypeptidase activity, aberrant cellular proliferation, reproductive
-carboxypeptidase activity, aberrant cellular proliferation, reproductive
-carboxypeptides, plum, small intestinal brain or proliferative. The BGS-42
-colypeptide, polynucleotide, or their modulators are also useful for
-creating infertility, cushing's syndrome, emphysema, pneumonia, Addison's
-creating infertility, cushing's syndrome, emphysema, pneumonia, Addison's
-creating infertility, cashing's syndrome, emphysema, pneumonia, Addison's
-creating infertility, astrhitis, asthma, Allos, sespis, and, sone, Sjogren's
-creating infertility, astrhity as a preventive agent for immunological
-colone sequence which is related to the invention.
                                                                                                                                                                                                                            testis-specific tubulin tyrosine-ligase-like polypeptide;
BGS-42 polypeptide; cytostatic; respiratory-Gen; gastrointestinal-Gen;
neuroprotective; endocrine-Gen; antinflammatory; anabolic; hypertensive,
osteopathic; nootropic; antiparkinsonian; antiarthritic; antiasthmatic;
anti-HIV; antibacterial; immunosuppressive; antiseborrheic;
dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase;
tubulin-carboxypeptidase; cellular proliferation; reproductive disorder;
testicular disorder; testicular cancer; pulmonary disorder; lung cancer;
gastrointestinal disorder; colon cancer; stomach cancer; neural disorder;
brain cancer; liver cancer; proliferative condition; testis; lung;
small intestine; brain; lymph tissue; infertility; Cushing's syndrome;
emphysema; pneumonia; Addison's disease; arromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; atthritis; asthma; AlDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, e.g. aberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sepsis; acne; Sjogren's disease; scleroderma; human; ds
                                                                                                                                                                                   Human BGS-42 protein-related DNA clone C SeqID11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO 11; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO.
                        ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-2002; 2002US-0394725P.
                        ADJ93363 standard; DNA; 3465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-2003; 2003WO-US021605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feder JN, Wu S, Nelson TC;
                                                                                                                                 (first entry)
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ADJ93363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCATCCACCTGTGCAACAAC
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                                                                                                                                                                                                                                                        81 AlavalGluAspLeuThrGluAlaGluTrpGluAspLeuThrGlnGlnTyrTyrSerLeu
                                                                                                                                                                                                                                                                                                                                                  ValHisGlyAspAlaPheIleSerAsnSerArgAsnTyrPheSerGlnCysGlnAlaLeu
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                                                                                                                                                                                                                                        AlaGluAsnAlaGluAlaLysLeuArgGlyLeuProGlyGlnLeuValAspIleAlaCys
                                                                                                                                                                                                                                                                                      LysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAsp
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T; 0 U; 0 Other;
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                                                          Conservative:
Mismatches:
 Sequence 3465 BP; 667 A; 1074 C; 1126 G; 598
                                                 Matches:
                                      Length:
                                                                                    Indels:
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2693.00
95.4%
95.4%
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Best Local Similarity:
                          Alignment Scores:
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SerLysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAsp

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MetAlaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArg

-153 21

Sequence 1939 BP; 421 A; 592 C; 589 G; 337 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches:

7.92e-166 2689.00 95.2% 95.2%

Indels:

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This invention relates to a novel testis-specific tubulin tyrosine-ligase—
like polypeptide, designated the BGS-42 polypeptide. The invention may
be useful for the development of compounds with a cytostatic, respiratory
CD be useful for the development of compounds with a cytostatic, respiratory
cantiparkinsonian, antiarthritic, antiasthmatic, antihacterial,
antiinflammatory, anabolic, hypertensive, osteopathic, nootropic,
antiinflammatory antiasthmatic, antiasthmatic, antihacterial,
immunosuppressive, antiseborrheic or dermatological activity acting as
tyrosine ligase modulators. In addition, the disclosed sequences may be
cc tyrosine ligase modulators. In addition, the disclosed sequences may be
useful for gene therapy. The BGS-42 polypeptide or polymolectide can be
used for diagnosing a pathological condition or a susceptibility to a
cused for diagnosing a pathological condition or a susceptibility to a
complicating a medical condition, such as a disorder related to aberrant
cubulin ligase activity, aberrant cellular proliferation, reproductive
carboxypeptidase activity, aberrant cellular proliferation, reproductive
disorders, testicular disorders, testicular cancer, pulmonary disorders,
lung canner, gastrointestinal disorders, scomeor, scomeor,
cof the testis, lung, small intestine, brain or lymph tissue. The BGS-42
cc polypeptide, polymolectide, or their modulators are also useful for
disease, acromegaly, Alzheimer's disease, or Parkinson's disease.
cc treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's
disease, acromegaly, Alzheimer's asthma, AIDS, sepsie, acromegaly, detect and
disorders including arthritis, asthma, AIDS, sepsie, acre, sjograe's
disease or scleroderma. The antibodise may be used to purify, detect and
ctarget the BGS-42 polypeptides are present sequence is that of a DNA
ccone sequence which is related to the invention.
emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease;
Parkinson's disease; immunological disorder; arthritis; asthma; AIDS;
sepsis; acne; Sjogren's disease; scleroderma; human; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 9; 343pp; English.
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                                                                                                                                                                                                                           Homo sapiens.
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ò	151		151
q	46443 AGTGTCTGTCCCTGCCCCTTCACTGAT	CTCTGTGTCCCCTCTGGGGTCTCAGAGGCTG	46384
ò	151		151
qq	46383 GTTCTGTTGGGGGAGGCCTGGGGGA	CTCAGGCACTGGCTTTAGCCTCATCCATGAGCGC	46324
ò	151		151
đ	46323 TAAGCCTTCCCTGCTCCCCCATCG	CCCCCACCAACCATGCTGCTGGTGGCCTTGGACAA	46264
ò	151		151
qu	46263 AGCCAGTGCAGGTCTCAGGGCCA	AGCCAGTGCAGGTCTCAGGGCCAAGCTGCGACCCTGCCCCAGGGCTCAGGAGCTCAGGTC	46204
ò	152		155
qq	46203 CCGCTGCACAGTGGCTGTGCATG	CCGCTGCACAGTGGCTGTGCATGCTGGGTTGAGCGGTGGCCTCTTGCAGACATAGTGTGC	46144
λo	26		175
අු			46084
충 음	176 AsnLysTrpValValGlnLysTy	AsnLysTrpValValGlnLysTyrIleGluThrProLeuLeuIleCysAspThrLysPhe	195 46024
ò	196 AsplicArgGinTrpPheleuVa		215
ą	46023 GACATCAGACAGTGGTTCCTCGT		45964
ò	216 GluserTyrLeuArgPheserThrGlnArgPheser	LeuAspLysLeuAsp	232
q	TTA	CTGGACAAGCTGGACAGGTCAGTG	45904
ò	232	2	232
qq	45903 CGGTGGCGACCTGGACACCTCGGGC	CAGGGAATGGGCTGCTGCTGCATGCCTGGAGCA	45844
ò	232		232
q	45843 GCCGCAGTGAGAAGCAGCACGGGCAGGGCCCCCTCACTGCCAC	CTGCCACCACGAGAGGC	45784
à	232		232
qq	45783 ACAGATGGGGAAACTGAGGCTTG	CTGAGGCTTGGGAGGCTGATGATCTCCCCGAGGGACAGGCCCAGGCC 4	45724
ò	232	2	232
QQ	45723 CACCGGCCTTCAAAGCCAGCGCC	CCGGCCTTCAAAGCCAGGGCCCTACACCCCACGCTCTGTGCATCATCTCTGGAAAATC 4	45664
ò	232	2	232
qq	45663 TTAAAAGGCACCATTTTGCCTGT	TTAAAAGGCACCATTTTGCCTGTGCCCAGGGGGATTGGAATGGTGGGCAGCACCTGGG 4	45604
'n	232	2	232
qq	45603 CCCTGGCGCAGGGGAGGCGGCCTGTGGGGTGCCTGGTGGAGG	3TGGGGTGCCTGGTGGAGGCTCAGATATCCGCAAGTG 4	45544
δ	232	2	232
ΩP	45543 TGCTGCCCAGGGTGGATGGACCCC	CCACCTCACCCGGGTCCCCGCGTGGGCAGGAGGGCGA 4	45484
8	232	2	232
qq	45483 GAGCCTGTGGAGTCCTCAGGAGT	CTCAGGAGTGTGCTGTGCACACAGCGACGCCTGCCACCCTCTGTCT 4	15424
δ	232	2	232
qq	45423 GCACCAAGGCTTCCTCTGACTAT	CTATTGTGTGGCCCTTGCTTGGTGTGAGGCGCTAGGGGACC 4	15364
ò	232	2	232

		Db 44283 TGGAGG	TGGAGGACACCGATCCTGCTCTGTGACCATGCTCGGTCCCGCTGAGGGCCCAGGCCTGCC 44224
g G	45363 TGACGGCTGGGCAGGAAGGGGTCTGCTTTTACGAGTGAGAATCCAGGGAGGCCCTGAGA 45304	773	373
ò	232 232	44223	CHARTICECE MARKETER FATHER CHECK ACCORACIO A A 164
අු	45303 GICACGCGACACACACACCTIGCAGGGGAGGITAACTCCGGCCCAGGCGAGCGGGTGCGGGTCA 45244		
δλ	232 232	2/2	できる (1977年)
q	45243 TGCCTGGTGGGTCATGCTCGAAGTCACACCCAGAAGAGGCCTGGGAGGAGCTGGCCAGGG 45184	T T T T T T T T T T T T T T T T T T T	
δ	232 232		THE CARGE CONTRACTOR ACTION CONTRACTOR AGAING CONTRACTOR A 1044
q	45183 GCTACGACCCTCACCTCACTCACTCGGTCAAGTGGGGCCTGGAGGGGGTCCAGGAAC 45124	521L	
δ	232 232	44043	CAGGCCACCTATGCTGCTTTGCCTTGGCCTGCAGTGCCTCCTCCACTCTGAGGATCT 43984
qa	45123 TCACCTGTGCAAAAGCAGCTCCCAGGCAGGGGAGTGAGAAGGCCAGGGGCCCCTGCCAGGG 45064	Qy 373	373
ò	232 232	43983	TTCGCGGGCCTCCCTGTGCCGGATGTGCTGGAGTCATTGGGAAGCGTGGCCAATGCC 43924
qq	45063 CCCATTTCTGGGCCTCCAGCTGTGAGCTGTGCGCCTGGCCAATCCCATGGCCTCTCTGAG 45004	373	373
ò		43923	TCTCTCTTGCGGCCTCTCTGTGGCTAAACTCGGGAAAAGAGCAGCTGAGTCCCTGGGTGT 43864
qq	45003 CCCTGTTTCTCCATCTGGGACAGTAACGCTCATCCCAGCTGGGCCCCTCCAGCAGAGGGT 44944	Qy 373	373
ò	232 232	43863	GGGGCCCCCCAGGCTGAAGCCTCAGGAAGCCTTGGTTCCCCGCAGGTTCTCCAG 43804
Dp	לז	Oy 373	373
δ	232 232	Db 43803 AGCCTG	AGCCTGGGGGCCTCCTGGGGGGTCTGCGTGGGACCCCCAGGTGTTCACTGTTCACTCCTGAG 43744
qa	44883 GACCGGCCTTGGGTGCCCTCCTGGGCCAAGGAGGCTGAGCACCTGCCCCTCGTCCCCCC 44824	Oy 373	373
č	SeralaileHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsnAspValGly	43743	TCAGGTGGGGGGTCTGTGCCCCGACCAGCCCCTCCTGCAGACCCCTCCTGCAGGGACCC 43684
q	TGCAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGGC	2y 374	GlnProValValGl 378
જે ક	252 ArgSerProLeuLeuProAlaHisAsnMerTrpThrSerThrArgPheGInGLuTyrLeu 271	Db 43683 CCCTA	NTCCCGGCCACAGCCCAGCACCTGTTCCTTCCCAAACCGGTGGTTGA 43624
g ò		378	upropropropheserGlySerAspLeuCysValAlaGlyValSerValArgArgAlaAr 398
QΩ	44703 CAGCGCCAGGGCCCGTGGCGCCGTGTGGGGGCGTCATCTACCCGTCCATGAAGGCC 44644	43623	
δ	IleAlaHisAlaMetLysValAlaGlnAspHisValGluProArgLysAsnSerPheGlu		
අ :		Oy 418 oLeuLy	OLeuLybAlaArgGlyProSerAlaMetProAspProAlaGlnGlyProProSerProAl 438
දු දු	11	43503	
λ̈		Qy 438 aLeuGl Db 43443 TCTCCA	aleudinArgAspleudiyleuLysGludiuLysGlyLeuProleurAlaueleuLarr 158
οp	44523 TCCAGCCCCACCATGCACCGTCCACGCCGGTCACGGCCCAGCTGTGCACACGTGCACAGGTGAGGGAGGGTGAGGGTGAGGGGGG	458	rgGlyAlaAlaGluSerGlyGlyAlaAlaGlnProThrArgThrLysAlaAlaGl 478
ò	GluAspThr11eLysValAlaValAspArgSerCysAsp11eGlyAsnPheGluLeuLeu 	43383	
අු :		Oy 478 YLYSVa	yLysValGluLeuProAlaCysProCysArgHisValAspSerGlnAlaProAsnThrGl 498
Š †	TrpArg	Db 43323 GAAGG	
8 &		Oy 498 yvalPr 	yvalprovalaladinproalalysSerTrpAspProAsnGlnLeuAsnAlaHisProLe 518
qq	44343 CTTTGCCACCTGGTCACTGGGGGGGGGGGGGGGCGGCCGCCAGTGCAGCGGGGGTCTA 44284	518	roValLeuArgGlyLeuLysThrAlaGluGlyAlaLeuArgProProGlyGl 538
δ,	373 373	43203	

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BGS-42 polypeptide, cytostatic; respiratory-Gen; gastrointestinal-Gen; neuroprotective; endocrine-Gen; antiinflammatory; anabolic, hypertensive; osteopathic; noctropic; antiparkinsonian; antiathritic; antiasthmatic; anti-HIV; antibacterial; immunosuppressive; antiseborrheic; dermatological; tyrosine ligase modulator; gene therapy; tubulin ligase; tubulin-carbox/peptidase; cellular proliferation; reproductive disorder; testicular cancer; pulmonary disorder; lung cancer; gastrointestinal disorder; colon cancer; pulmonary disorder; lung cancer; paran cancer; lung cancer; proliferative condition; testis; lung; small intestine; brain; lymph tissue; infertility; Cushing's syndrome; emphysema; pneumonia; Addison's disease; acromegaly; Alzheimer's disease; Parkinson's disease; immunological disorder; archiritis; acthma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New testis-specific tubulin tyrosine-ligase-like BGS-42 polypeptide, useful for preventing, treating or ameliorating a medical condition, eaberrant cellular proliferation, reproductive disorders or testicular
                                                                                                                                                                                                                                                                                                                                                                                           sepsis; acne; Sjogren's disease; scleroderma; human; gene; ss.
                                                                                                                                                                                               testis-specific tubulin tyrosine-ligase-like polypeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Human BGS-42 protein"
/partial
/note= "No start or stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .726
                                                                                                                                                                     CDNA sequence SeqID3
                                                                               ADJ93359 standard; cDNA; 726
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YLYSGLYSer 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004005487-A2
                                                                                                                                                                     BGS-42
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                        43143
                                                                                                            ADJ93359;
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carboxypeptidase activity, aberrant cellular proliferation, reproductive disorders, testicular disorders, testicular cancer, pulmonary disorders, lung cancer, gastrointestinal disorders, colon cancer, stonach cancer, neural disorders, brain cancer, liver cancer, or proliferative condition of the testis, lung, small intestine, brain or lymph tissue. The BGS-42 polypeptide, polymucleotide, or their modulators are also useful for treating infertility, Cushing's syndrome, emphysema, pneumonia, Addison's disease, acromegaly, Alzheimer's disease, or Parkinson's disease. The BGS-42 polypeptide can be used as a preventive agent for immunological disorders including arthritis, asthma, Allos, sepsis, acne, Sjogren's disease or scleroderma. The antibodies may be used to purify, detect and target the BGS-42 polypeptides. The present sequence is that of a partial cDNA which encodes the human BGS-42 protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ATAGTGTGCATGGAGCAGGAGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTT
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Mismatches:
Indels:
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This invention relates to a novel testis-specific tubulin tyrosine-ligase-like polypeptide, designated the BGS-42 polypeptide. The invention may be useful for the development of compounds with a cytostatic, respiratory-Gen, gastrointestinal-Gen, neuroprotective, endocrine-Gen, antinflammatory, anabolic, hypertensive, osteopathic, nootropic, antiparkinsonian, antiarthritic, antiasthmatic, anti-HIV, antibacterial, immunosuppressive, antiseborrheic or dermatological activity acting as tyrosine ligase modulators. In addition, the disclosed sequences may be used for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, and for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant tubulin ligase activity, a disorder related to aberrant tubulin-

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(CYSKP) and their associated polynucleotide sequences. The sequences are useful in the treatment of disorders associated with overexpression or underexpression of CYSKP in a patient. The disorders include cell

cuderative disorders (such as cancer, actinic keratosis, arteriosclerosis, cirrhosis, hepatitis and psoriasis),

arteriosclerosis, Crohn's disorders (such as, asthma, atherosclerosis, osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus

and anaemia), vesicle trafficking disorders (such as, asthma, diabetes insipidus, Grave's disease and goitre), gastrointestinal disorders, prion diseases, neurological disorders (such as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease, and other motor neuron disorders), cell motility disorders, reproductive disorders (such as endometriosis and polycystic ovary syndrome), muscle disorders (such as endometriosis and polycystic ovary syndrome), muscle diseases, central nervous system disorders (such as bown syndrome and creable infarction, epilepsy and muscular dystrophy), spinal cord diseases, central nervous system disorders (such as anxiety and schizophrenia). Sequences AASS9890-AAS99823 represent cDNA molecules encoding human CYSKP of the invention
                                                                                                                                                                                                                                                                                                                                                                        Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder; ss; cell proliferative disorder; inflammatory disorder; prion disease; vesicle trafficking disorder; gatrointestinal disorder; muscle disorder; neurological disorder; cell motility disorder; reproductive disorder; spinal cord disease; central nervous system disorder; mental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baughn MR, Hillman JL;
Burford N, Batra S, Kearney L;
                                                                                                                                                                                                                                                                                                                          Polynucleotide encoding human cytoskeleton-associated protein (CYSKP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cytoskeleton-associated proteins and polynucleotides, useful for diagnosing, preventing and treating cell proliferative, autoimmune, inflammatory, neurological, cell motility, reproductive and muscle
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Y, Lal P, Yao MG, Bandman O,
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                                                                                                                                                                 AAS99894 standard; cDNA; 2380 BP
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08-MAY-2000; 2000US-0202729P.
05-JUN-2000; 2000US-0209705P.
07-JUN-2000; 2000US-02149P.
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                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; cancer.
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ArgGln 374
                                                     AGGCAG 726
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Azimzai Y,
Policky JL;
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 U; 0 Other;
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250
81
198
76
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                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
670 G; 445 T; 0
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   580 A; 685
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1070.50
54.8%
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   Sequence 2380
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HisValGluProArgLysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGlyArg
                                                                           AspPheArgProTrpLeulleGlulleAsnSerSerProThrMetHisProSerThrPro
                                                                                                                                                                                                                                     378 GluProProPheSerGlySerAspLeuCysValAlaGlyValSerValArgArg---
                             1158 ACCGFGCAGTGTCGGAAGGCCCAGCTTTGAGCTCTATGGCGCTGACTTCGTGTTCGGGGAG
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AGGTCAAGGC 2063
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The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polymucleotide omprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 5'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the combination of the 5'-end sequence)3'-end sequence is selected from those defined in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification. The primers erg can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13612 represent human amino acid sequences; AAB92446 to AAB92446 to AAB92893 represent human amino acid sequences. And AAH13629 to AAH13621 represent oligonucleotides, all of which are used in the exemplification of the
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                         88.
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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                   detection; diagnosis; antisense therapy; gene therapy;
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, Otsuki
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Matches:
Conservative:
Mismatches:
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Sugiyama T, Wakamatsu A, Nagai K,
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Gaps:
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2000JP-00118776.
2000JP-00183767.
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                     primer;
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                                                        Homo sapiens.
                                                                                                                                                                                                                                           11-JAN-2000;
02-MAY-2000;
                                                                                            EP1074617-A2
                                                                                                                                                                                                        29-JUL-1999;
27-AUG-1999;
                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                           Ota T, IE
Ishii S,
                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
g
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. 4.

Human cDNA sequence SEQ ID NO:15920

(first entry)

26-JUN-2001

AAH16735

cumour specification (or their complements, degenerate variants, sequences consisting of at least 20 contiguous residues them, sequences consisting of at least 20 contiguous residues them, sequences consisting of at least 20 contiguous residues them, sequences charby byridises to them under highly stringent conditions or sequences having at least 75 or 90% sequence identity to the 1855 sequences. Also included are detecting/determining the presence of cancer in a patient, at solated an immune response in a patient; treating kidney cancer in a patient, an isolated antibody (or its antigen-binding fragment) that expression control sequence, a host cell transformed/transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the protein, a fusion protein comprising at least one the proteins, an isolated Treall population comprising the T-cells specific for a tumour protein, an isolated T-cell population comprising the T-cells, a composition comprising a first component (such as a carrier or immunostimulant) and a second component (such as a carrier or composition comprising at least one of the oligonucleotides, or at least one of the oligonucleotides, or at least one of the oligonucleotide, or a least one of the oligonucleotide, or at least one of the oligonucleotide, or at least one of the oligonucleotide, or at least one of the printing and/or expanding T-cells specific for a tumour protein, and stimulating and/or expanding T-cells specific for a tumour protein, and stimulating and/or expanding T-cells specific for a tumour protein, and stimulating indumer response in a patient. The present component is sequence at so this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence of the detection them. The invention relates to a new isolated polynucleotide (a Human kidney tumour specific cDNA) comprising any one of the 1855 sequences identified seqdata.uspto.gov/sequence.html?DocID=20030109434. invention relates to a new isolated 85939999999999999999999999999

Sequence 2538 BP; 555 A; 717 C; 734 G; 532 T; 0 U; 0 Other;

Alignmen	Alignment Scores:			
Pred. No.:		5.59e-57	Length:	2538
Score:		1020.00	Matches:	220
Percent	Percent Similarity:	55.5%	Conservative:	69
Best Loo	Best Local Similarity:	42.28	Mismatches:	151
Query Match:	atch:	35.78	Indels:	81
DB:		7	Gaps:	12
US-10-6	US-10-635-977-2 (1-541) x ADS73168 (1-2538)	x ADS73168	(1-2538)	
ò	54 GlnLeuVal	AspileAlaCys	54 GlnLeuvalAspIleAlaCysLysValCysGlnAlaTyrLeuGlyGlnLeu	reuGlyGlnieu
DP	835 GAGTTTGTC	 GATGAAGCTCTG	::: 835 GAGTITGIGGANGAAGCTCTGTGTGCGTGCGAGGAGTACCTTAGCAACTTG	 CTTAGCAACTTG
Ġ	74 AspileAst	ThrSerAlaAsp	74 ครุกเคครุกาหรอาการสมุลกรุกใส่ขอได้ในครุกเคนาหัวในคายนา	GluAlaGluTrp
qq	895 GACATOGAC	:::	 -	

1015 GTCCAGCGCTGTGAGGACATCCTGCAGCAGCTGCTGGTACCCCCAGATAGACATG 1074 CTCCAGCGCTACTACCAAGTGGTCCACGAAGGGGCAGAACTCAGGCACCTCGACACTCAG 1014 94 ThrGlnGlnTyrTyrSerLeuValHisGlyAspAlaPhelleSerAsnSerArgAsnTyr 113 114 PheSerGlnCysGlnAlaLeuLeuAsnArgIleThrSerValAsnProGlnThrAspIle 133 134 AspGlyLeuArgAsnIleTrplleIleLysProAlaAlaLysSerArgGlyArgAspIle 153 193 LysPheAspIleArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPhe 213 154 ValCysMetAspArgValGluGluIleLeuGluLeuAlaAlaAlaAspHisProLeuSer 173 GACATCGACAAGGACCTGGAGGCCCCGCTGTACCTCACCCCCGAGGGCTGGTCCCTCTTC 954 GCCCACATG 894 GluHisGlu 73 GluAspLeu 93 ArgAspAsnLysTrpValValGlnLysTyrIleGluThrProLeuLeuIleCysAspThr 174 1195 1255 194 g ઠે g ઠે ઠ a ઠે 셤 à 셤 δ

ò	ы	233
Db	1315 TACCGCGACAGCTATATCCCGCTTTTCCACGCGCCTTCTCCCCTGAAGAACCTGGACAAC	1374
ò	lalleHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsnAspValGlyArgSer	253
Ωp		1434
ò	roLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArg 	273
В		1494
λ̈́o		293
qq	1495 ATGGCTCCAAATGCTTCGTCCACCATCATCGTGCTGGCATGAGGATGCTGTGATC	1554
ò		313
Dp	1555 CACGCACTTCAGACCTCCCAGGACACCGTGCAGTGTCGGAAGGCCAGCTTTGAGCTCTAT	1614
ζ	314 GlyAlaAspPheValLeuGlyArgAspPheArgProTrpLeuIleGluIleAsnSerSer	333
Dp	1615 GGCGCTGACTTCGTGTTCGGGGAGGACTTCCAGCCTGGTTGAGATCAACGCCAGC	674
ò		353
DP QC	1675 CCCACGATGGCACCCTCCACAGAGTCACTGCCCGGCTCTGTGCTGCGCGTGCAAGCTGAC	7
ò	gSerCysAspileGlyAsnPheGl	69
DÞ	1735 ACCTGGGGTGGTCATTGACCGGATGCTGGACCGCAACTGTGACACAGAGCCTTTGAG	794
ò	oValValGluPro-	88
DÞ	:::::::	843
ć	lSerValArgArgAlaArgArgGlnValLeuP	80
qq	1843	843
à	Ja	28
qq	1844CCAGCTGCCTTCTCCCCATGTACTCCGACACCAGGGCCAGGTCCTCAGACGACGACG	899
ò	spProAlaGlnGlyProProSerProAlaLeuGlnArgAspL	48
Dþ	1900 ACAGCAGCTGGTGGGCACTAAGGCCCTGTCGACCACGCAAGGCCTTGAGGACTC 1	926
à	448 uLysGlyLeuProLeuAlaLeuLeuAlaProLeuArgGlyAla 4	62
DÞ	1957 TACCCACGGCTAAGGTCTTCATTTCCCTCCCACGAACCTTGATTTCAAGGTGGCACCCA 2	910
ò	463AlaGluSerGlyGlyAlaAlaGlnProThrArgThr	74
Dþ	2017 GCATCCTGAAGCCAAGAAAGGTGGGCCTCGACCTGTGACTCACACCCAGTGGACAGTGCT 2	920
ò	475	88
qq	2077 GAGCACGGGGTCAGGGCTGGAGGGCACAGGCAGAGGCGGCGCCCAGGCTGG 2	128
à	488 gHisValAspSerGlnAlaProAsnThrGlyValProValAlaGlnProAlaLysSerTr	80
QQ	2129CTGGCACCCCAAGGGAAGAGCTG	151
à	508 pAspProAsnGlnLeuAsnAlaHisProLeuGluProValLe 5	22
QQ	υ	211
δ	522 uArgGlyLeuLysThrAlaGluGlyAlaLeuArgProProProGlyGl 5	38
QQ	2212 TTCACACCGAGGCTCCTGCTCCTGTGCCTCCGAGGCCCCCAGCTGG 2	259

734 G; 532 T; 0 U; 0 Other;

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Sequence 2538 BP; 555 A; 717 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a new isolated polynucleotide (I) comprising: any one of the 1855 sequences identified in the specification; complements or degenerate variants of (a); sequences consisting of at least 20 contiguous residues of (a); sequences that hybridize to (a) under highly stringent conditions; or sequences that hybridize to (a) under highly stringent conditions; or sequences that hybridize to (a) under highly stringent conditions; or sequences that hybridize to (a) an immune response in a patient; strinmlating (M1) or determining the persence of cancer in a patient; strinmlating (M1) or determining the polypeptide (II) encoded by (I) and comprising, or having at least 70 or oplypeptide (II) encoded by (I) and comprising, or having at least 70 or specification; an expression vector (III) comprising (I) operably linked to an expression control sequence; a host cell (IV) transformed or transfected with (III); an isolated antibody (V) or its antigen-binding fragment that specifically binds to (II); a fusion protein (VI) comprising at least one (II); an oligonucleotide (VII) that hybridizes to the nucleotide sequences cited above under highly stringent conditions; simulating (M4) and/or expanding T-cells specific (VII) that hybridizes to composition (IX) comprising a first component such as a carrier or composition (IX), or an antigen-binding fragment that expection composition (VII), or an antigen-binding fragment that composition as second component composition or at least one antibody and a least one of the oligonucleotide, or at least one antibody and a least one of the oligonucleotide, or at least one antibody and a least one of the oligonucleotide, or at least one antibody and a least one of the oligonucleotide, or at least one antibody and a least one of the oligonucleotide, or at least one antibody and a least one of the oligonucleotide, or at least one purposenting and/or expanding T-cells specific for a tumor or propermy and stimulating immune response in a patient. This sequence represents a k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynuclectides and polypeptides, useful for detecting the presence of, and treating cancer, particularly kidney cancer by stimulating T-cells specific for a tumor protein, and stimulating immune response in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; pharmaceutical; cancer; cytostatic; disease; neoplasm; renal tumor; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon B, Harlocker SL;
                                                                                                                                                                                                                                                                                                                                                             cDNA elevated in kidney tumor cells SEQ ID NO 1765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; SEQ ID NO 1765; 252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaiger A,
                                                                                                                                                                                   ADW42022 standard; cDNA; 2538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2001; 2001US-0277245P.
21-DEC-2001; 2001US-0343340P.
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                                                                                                                                                                                                                                                                                                   (first entry)
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         538 y 538
                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy;
genitourinary
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                                                                                                                                                                                                                                                ADW42022;
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1674
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                                                                                                                                                                                                                                                                                    274 GlnGlyArgGlyAlaValTrpGlySerValileTyrProSerMetLysLysAlalleAla 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrLysGluSerTyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAspSer 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AlaileHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsnAspValGlyArgSer 253
                                                                                                                                                                                                                                                                94 ThrGlnGlnTyrTyrSerLeuValHisGlyAspAlaPhelleSerAsnSerArgAsnTyr 113
                                                                                                                                                                                                                                     74 AspileAspThrSerAlaAspAlaValGluAspLeuThrGluAlaGluTrpGluAspLeu 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 HisAlaMetLysValAlaGlnAspHisValGluProArgLysAsnSerPheGluLeuTyr
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                                                                                                                                                                                                                                                                                                                                                                                        134 AspGlyLeuArgAsnIleTrpIleIleLysProAlaAlaLysSerArgGlyArgAspIle
                                                                                                                                               54 GlnLeuvalAspIleAlaCysLysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGlu
                                                                                                                                                                                                                                                                                                                               114 PheSerGlnCysGlnAlaLeuLeuAsnArgIleThrSerValAsnProGlnThrAspIle
           2538
220
69
151
81
         Length:
Matches:
Conservative:
Mismatches:
                                                                      Indels:
                                                                                                                    US-10-635-977-2 (1-541) x ADW42022 (1-2538)
         5.59e-57
1020.00
55.5%
42.2%
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                                            Percent Similarity:
Alignment Scores:
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2016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
LeuLeuTrpArgGlnProVal - - - ValGluPro - ProProPheSerGlySerAspLeuCy
                                                                                                         sValAlaGlyValSerValArgArgAlaArgGrnValLeuProValCysAsnLeuLy
                                                                                                                                                                                                                                                                                                                                  1957 TACCCACGGCTAAGGTCTTCATTTCCCTCCCACCGAACCTTGATTTCAAGGTGGCACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TCACCGAAGGCTCCTGCTCTCTGTGCCTCCGAAGGCCCCCAAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LysAlaAlaGlyLysValGluLeuProAlaCysProCysAr
                                                                                                                                                                                                                                     428 oAspProAlaGlnGlyProProSerProAlaLeuGlnArgAspLeuGlyLeuLysGluGl
                                                                                                                                                                                                                                                                                                     448 uLys-----GlyLeuProLeuAlaLeuLeuAlaPro---LeuArgGlyAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2077 GAGCACGGGGTCAGGGCTGGAGGCCACAGGCAGAGGGCAGGCTCCCAGGCTGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 gHisValAspSerGlnAlaProAsnThrGlyValProValAlaGlnProAlaLysSerTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 pAspProAsnGlnLeuAsn------AlaHisProLeuGluProValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uArgGlyLeuLysThrAlaGluGlyAlaLeuArgPro------ProProGlyGl
                                                                                                                                                                                                                                                                                                                                                                   463 -----AlaGluSerGlyGlyAlaAlaGlnProThrArgThr-----
                                                                         crcarcraraagcagcccgrcaccacrrccccagccrccacaaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN37881 standard; cDNA; 2553 BP
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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are coverexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide and polypeptide and teate 80% identical to the TAT nucleic acids and polypeptides expression vectors and host cealls comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or antibodies, antagonists, binding molecules and compositions are useful antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, cancers of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2553 BP; 575 A; 716 C; 733 G; 529 T; 0 U; 0 Other;
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02-OCT-2002; 2002US-0414971P.
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

wulnerary; antipsoriatic; antiparkinsonian; nootropic, neuroprotective;
wulnerary; antipsoriatic; antiparkinsonian; nootropic, neuroprotective;
wintionulant; otheromolytic; coaquiant; ammunosuppressant; cardiant;
immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic;
whypotensive; dermatological; immunosuppressive; antiinflammatory;
antiviral; antibacterial; antifungal; antithuematic; antithyroid;
wn antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
candiovascular disease; diabetes mellitus; hypothyroidism; SCID; ALDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
whome damage; cartilage damage; antiinflammatory disease; coaquiation;
thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX agueunces have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; antiviral; antifungal; antitheumatic; antihifammatory; antibacterial; antiviral; autitheumatic; antihifammatory; antibacterial; to yor preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX
                                                                       -- ProProGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                           Human ORFX ORF2769 polynucleotide sequence SEQ ID NO:5537.
                                                 522 uArgGlyLeuLysThrAlaGluGlyAlaLeuArgPro
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                                                                                                                                                                                                              AAC77214 standard; cDNA; 2881 BP.
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名 3	Human polynucleotide SEQ ID NO 809.
\$ & &	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CMS;
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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Best Local Similarity:
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                                                   WO200153312-A1
                                                                                                                                       23-DEC-1999;
21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
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2144	354	2204	370	2264	388	2312	408	2313	428	2369	448	2426	46	248	475	2546	488	2598	20	2621	52	2681	53	2729	,
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Search completed: April 4, 2006, 10:34:27 Job time : 864 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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osing. Grame plus pend nucleic search, OM protein

(without alignments) 3892.697 Million cell updates/sec ; Search time 7900 Seconds April 4, 2006, 09:36:08 Run on:

1 MASSILKWVSHQSCSRSSR.....LRGLKTAEGALRPPGGKGS US-10-635-977-2 2854 score: Sequence:

541

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

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GenEmbl:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AL022327 Human DNA	CQ724907 Sequence	יקשם סוווסוו בכבבבחים
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ALIGNMENTS

HS355C18 101270 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RP3-35SC18 on chromosome 22q13.3 Contains the KIAA0027 gene, ESTs, STSs, GSSs and seven putative CpG islands, complete sequence.
AL022327
AL022327.17 GI:5304851
HTG; CpG island; KIAA0027.
Homo sapiens (human) RESULT 1 HS355C18/c LOCUS DEFINITION

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 101270)

Cobley, V AUTHORS TITLE JOURNAL

COMMENT

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REFERENCE

Submitted (13-MMY-2005) Wellcome Trust Sanger Institute, Hinxton, Submitted (13-MMY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 30, 1999 this sequence version replaced gi:5262834.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

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46923 GGCGTGGGGGTCAGGACTCAGGCGCTGGAGCTGGAGGCGTCTTCACAGCATGTGT 46864
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                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
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                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="RPCI-3"
                                                                                                                                             --- Genome Center
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151

46924

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Dp	46863 TCCGATCACAGGAGCAAGGATCCGGGTTGATCACGTTAATCACGATTTAATCTACGATTTAATCACAATTTCAAAAGATTCAAAAAAAA	QQ	45783 ACAGATGGGGAAACTGAGGCTTGGGAGGCTGATGATCTCCCCGGAGGGACAGGCCCAGGCC 45724
Š		ò	232 232
3 음	46803 CAAACIGGICIAIGCITIICCITITIAGIITITIAITITIAITITITAATITITIAGIITITI 46744	qq	45723 CACCGGCCTTCAAAGCCAGCCCCTACACCCCCACGCTCTGTGCATCATCTCTGGAAAATC 45664
ò		δ	232 232
qq	46743 TGAAACGGAGTTTCACTCTTGTTGCCCAGGCTGAAGTGCAGTGGCGCAATCTTGCCTCAC 46684	qq	45663 TTAAAAGGCACCATTTTGCCTGTGCCCAGGGGGATTGGAATGGTGTGGGCAGCACCTGGG 45604
Š		ò	232 232
ପ୍ର	TGCAACCTCCACCTTCCAGGTTTAAGCAATTCTCCTGCCTTAGCCTCCCAAGTAGCTGGG	qq	45603 CCCTGGCGCAGGGGGGGCCCTGTGGGGTGCCTGGTGGAGGCTCAGATATCCGCAAGTG 45544
ò		ò	232 232
q	46623 ACTACAGGCGCCCACCACCACACCGGCTAATTTTTTTTTT	а	45543 TGCTGCCCAGGTGGATGGACCCCCACCTCACCCGGGTCCCCGCGTGGGCAGGGGGGG 45484
ò	!	ò	232 232
· අ	CCATGTTGGCCAGGCTGGTCTTGAACTCCCGACCTCAAGTGATTCACCTGCCTCGGCCTC	qq	45483 GAGCCTGTGGAGTCCTCAGGAGTGTGCTGTGCACACAGCGACGCCTGCCACCCTCTGTCT 45424
ò		ò	232 232
q	46503 CCAAAGTGCTGGGATTACAGGCATAAAGCCACCATGCCCATCCTCCTGGCTCCCTTTTAAA 46444	g	45423 GCACCAAGGCTTCCTCTGACTATTGTGTGGCCCTTGCTTG
ò	151 151	δ	232 232
qq	46443 AGTGTCTCTGTCCCTGCCCCTTCACTGATCTCTGTGTCCCCTCTGGGGTCTCAGAGGCTG 46384	අු	45363 TGACGGCTGGGCAGGAAGGGGGTCTGCTTTTTACGAGTGAGAATCCAGGGAGGCCTGAGA 45304
à	151	ò	232 232
' සි	GTTCTGTTGGGGGAGAGCCTGGGGACTCAGGCACTGGCTTTAGCCTCATCCATGAGCGC	Op	45303 GTCACGCGACACAGACCTTGCAGGGGAGTTAACTCCGGCCCAGGCGAGCGGCTGCGGTCA 45244
ò		à	232 232
යු	TAAGCCTTCCCTGCTCCCCATGGCCCCAACCATGCTGCTGCTGGCTG	Ор	45243 TGCCTGGTGGGTCATGCTCGAAGTCACACCCAGAAGAGGCCTGGGAGGAGCTGGCCAGGG 45184
Š		ò	232 232
: A	AGCCAGTGCAGGTCTCAGGGCCAAGCTGCGCCCCAGGGGTCAGGAGCTCAGGTC	ф	45183 GCTACGACCTCACTGCTCACTGCTCTGGTCAAGTGGGGCCTGGAGGGGGTCCAGGAAC 45124
ò	AsplieVal	ò	232 232
; 음	CCGCTGCACAGTGGCTGTGCATGCTGGGTTGAGCCGGTGGCCTCTTGCAGCATAGTGTG	q	45123 TCACCTGTGCAAAAGCAGCTCCCAGGCAGGCAGTGAGAAGCCAGGGCCCCCTGCCAGCG 45064
Š	Met Asparaval Gluglut lefenglufenal ab laban His Droten Sorbrasen	ò	232 232
; 음		QQ	45063 CCCATTTCTGGGCCTCCAGCTGTGAGCTGTGGGCCTGGCCAATCCCCATGGCCTCTGAG 45004
ò	AsnivsTrpValValGlnLvsTvrIleGluThrProLeuLeuIleCvsAsoThrIvsPhe	ò	232 232
. A		qq	CCCTGTTTCTCCCATCTGGGACAGTAACGCTCATCCCAGCTGGGCCCCTCCAGCAGAGGT
ò	196 AspileArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLys 215	හි :	
qq	_8_	g 8	TGGAGTCCTCAGGGGCAGGGTTCTCTAGAGCCAGCTGGGGTGGGCTCAGCACGGCTGGGAG
ò	216 GluSerTyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAsp 232	පි සි	CASIS A CHARLOS CASIS CA
Dp	45963 GAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGGTCAGTG 45904	g (GACCGGCCTTGGGTGCCCTCCTGGGCAAGGGAAGCTGAGCACCTGCCCCTCCTCCCCCCCC
ò	232 232	රි සි	233SerAlalleHisLeucysAsrAsrAshaNalGinLysTyrLeuLysAsrAspValGly 251 44823 #GAGGGGARGARGARGARGARGARGARGARGARGARGARGA
qq	45903 CGGTGGGCGACCTGGACACCTCGGGCCAGGGATGGGCTGCTGCTGCATGCCTGGAGCA 45844		16CAGCCCCA1CCACCTG1GCAACAACGCCG1CCAGAAGTACTACCTGAAGAATGGTGATGTGGGC
ò	232	중 음 전	25.4 ArgbertzoleuLeukrokaantakanmetirpintserintargenegingiutyrteu 271 44763 CGCAGCCCCTGCTGCCCCCACAACATGGAACAGGACCAGGACCAGGATCCAGGAGTACCTG 44704
<u>a</u>	GCCGCAGTGAGAAGCAGGGCAGGGCCCCCTCACTGCCACCTGCCACCACGAGAGGC	ò	272 GlnArgGlnGlyArgGlyAlaValTrpGlySerValIleTyrProSerMetLy8Ly8Ala 291
ò	23.2 23.2	QQ	44703 CAGCGCCAGGCCCCGTGTGGGGCGCAGCGTCATCTACCCGTCCATGAAGAAGGCC 44644

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Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                               / trains lation="MDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQVQR
CEDILQQLQAVVPQI DWEGDRNIWIYWCGAKSRGRGIMCMDHLEBMLKLWGNPVWMK
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RRWGYRPAVPLLTQRGSGRARHFPSLHTKAQLESPHVLRHQGQVLRRQHSKLVGKKA
LSTTGKALRTLDRAKVFISLPPNLDFKVAPSILKFRRKQLDL"
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                                                                                                    /mol type="mina" septemb
/mol type="mina" septemb
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/clone_lib="586 (synonym: hutel). Vector pSportl; host
DH108; sites NotI + SalI/MluI"
| 40.9 stage="adult"
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                                                                                                                                                                                                                                             1540. .2844
/gene="DKFZp586B0320"
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239
88
182
86
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1540. .2844
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S. Direct Submission
Submission
Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS,
Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPS); Email B. wiemann@dkfz-heidelberg de;
sequenced by AGOWA (Berlin/Germany) within the CDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                               LysProAlaAlaLysSerArgGlyArgAspIleValCysMetAspArgValGluGluIle
                                                                     AAGCCCGCGGCCAAGTCCCCGGGGCCGAGACATAGTGTGCATGGACCGTGTGGAAGGAGATC
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Oy 466 lyGlyalaAlaGlnProThrArgThr	Db 2887 AGGCACAGGCAGGCTGCTCCAGGCTGG	515AlaHisProLeuG ::: 2962 CCTCCACAGACTTCTGATCATCTCCTCTT	CCCCAGCTGGA 30	9 EH	2	Eukar Mamma Homir	KEFEKENCE 1. Tang, Y.T., Au-Young, J., Lu, D.A., Baughn, M.R., Hillman, J.L., AUTHORS Yue, H., Tang, Y. Tao, M.G., Bandman, O., Burford, N., Batra, S., Keatrney, L. and Pollocky, J.L. And Pollocky, J.L. A. Tang, P. Tang	AL S		IN Iment Scores:	Pred. No.: 4.05e-47 Length: 2380 Score: 1070.50 Matches: 250 Percent Similarity: 54.8\$ Conservative: 81 Best Local Similarity: 41.4\$ Mismatches: 198 Onerv Match: 37.58 Indels: 76	6 Gaps: -635-977-2 (1-541) x AX301197 (1-2380)	Qy 2 AlaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerSerArgSer 21	Qy 22 LysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAspAla 41	Qy 42 GluasnalaGlualaLysLeuArgGlyLeuProGlyGlnLeuValaspIleAlaCysLys 61 :::	Qy 62 ValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAspAla 81
	Ileneululeukilaalaakaphibrocheuseraagasphshipviluyalaululeukileukileukileukileukileukileukile	1867 AAGTATATTGAGGGGCCCCTCCTCATCTTTGGCAGGTTTGACCTCAGALAGTGGTTT 1920 202 LeuvalthraspTrpasnProLeuthr1leTrpPheTyrLysGluSerTyrLeuArgPhe 221 1927 CTGGTAACTGACACCCACTTACCGTGGGTTCTACCGCGACGGTATATCCGCTTT 1986	222 SerThrGlnArgPheSerLeuAspLysLeuAspSerAlaileHisLeuCysAsnAsnAla 241	242 ValGlnLygTyrLeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsnMet 261 ::: ::	262 TrpThrSerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGlyAlaValTrpGly 281	282 SerVallleTyrProSerMetLysLysAlaileAlaHisAlaMetLysValAlaGlnAsp 301 :::::	302 HisValGluProArgLysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGlyArg 321 :::	322 AspPheArgProTrpLeulleGlulleAsnSerSerProThrMetHisProSerThrPro 341	342 ValThralaGlnLeuCysAlaGlnValGlnGluAspThrIleLygValAlaVal 359 	360AspargSerCysAspIleGlyAsnPheGluLeuLeuTrpArgGlnProValVal 377		398 Arg	409 AlaSerAlaSerLeu-LeuAspAlaGlnProLeuLysAla-ArgGlyProSerAlaMet- 427	428 ProAspProAlaGlnGlyProProSerProAlaLeuGln 440 2647 CCCATGTACTCCGACACCAGGCCAGGTCCTCAGACGACAGCAAGCTGGTGGGC 2706	441GlyLeuP 452 2707 ACTAAGGCCTGTCGACCACGGCTAAGGCCTTGAGGACTCTACCCACGGCTAAGGTCTTC 2766	452 roLeuAlaLeuLeuAlaProLeuArgGlyAlaAlaGluSerG 466

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Wagner, L., Shenmen, C.M., Schuler, G.D., Betcw, K.H., Schaefer, C.F., Bhat, N.K., Te, T., Max, S.I., Wang, J., Haleh, F., Rarner, A.A., Rubin, G.M., Hong, L., Mando, M.F., Casavant, T.L., Usdin, T.B., Toshiyuki, S., Loquellano, N.A., Peters, G.J., S.S., Loquellano, N.A., Peters, G.J., A.M., Gay, L.J., Hulyk, S.W., Odergren, E.J., Hulyk, S.W., Odergren, E.J., Lu, X., Gibbs, R.A., A.M., Madan, A., Rodrigues, S., Mach, Young, A.C., Shevchenko, Y., Touchman, J.W., Green, B.D., Grimwood, J., Schmutz, J., Myers, R.M., M.I., Skalska, U., Smailus, D.E., nes, S.J. and Marra, M.A. igase-like family, member 3, Aclone MGC:120531 IMAGE:4002561), GAAGCCAGTCTCCACTGCCACTTCAGCC 1637 GATTGCCACTGAGTCCGAAGAACCCCCCAGGC 1816 CGAGTGTTCCAAGGCGATTTATTCCTGCTCT 1876 AAGGGCCACAGCCCTGGTCTGCCCCAATCTC 1697 CACCCACCAAAGAGCCACCAGTAGCAAGTA 1936 AAATACACAGCCAAATTAGCTGGGCACGGTG 1996 |||| AGGCTAATGAGGAT---CGCTTGAGCCCGGG 2053 laCysProCysArgHisValAspSerGlnAl 494 laGlnGlyProProSerProAlaLeuGln-- 440 lyLeuProLeuAlaLeuLeuAlaProLeuAr 460 ------ProAlaLy 506 isPro----- 517 raniata, Vertebrata, Euteleostomi, lires, Primates, Catarrhini; hralaGluGlyAlaLeuArgProProGl Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) JOURNAL

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K.,
Blakesley,R.W., Bouffard,G.G., Breen,K.,
Dietrich,N.L., Granite,S., Cunn,X., Gupta,J., Haghighi,P.,
Dietrich,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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LSTTGKALRTLPTAKVPISLPPNLDFKVAPSILKPRKVGLDL"
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAM Plate: 4 Row: p Column: 9.
Location/Qualifiers
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                                                                             Submitted (10-JUN-2005) National Institutes of Health,
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
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Is (bases 1 to 2326)

So Cat.7., Isogai.7., Nahikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof.
Primer for synthesizing full-length cDNA and use thereof.

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/13570
PD 09-JUL-2002
PP 28-JUL-2000
PP 28-JUL-2000
PP 28-JUL-2000
PP 28-JUL-2000
PP 28-JUL-2000
PP SAITO,
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC C12N15/09,CO7K14/47,CO7K16/18,C12N1/15,C12N1/21,C12N5/PC
GCAGTCCCTCTGCTGACCCAGCGAGGCTCTGGGGAAGCCCGTCACCACTTCCCCAGCCTC 1442
                                                                                                                                                            1563 ACTCTACCCACGGCTAAGGTCTTCATTTCCCTCCCACCGAACCTTGATTTCAAGGTGGCA 1622
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1758 GCTGGTCCCCCCCAGAAGCCCCTTCCTCAGACTTCTGATCATCTCCCCTCTTCTCCCC 1817
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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1503 CGACAGCACAGCAGAGCTGGGGCACTAAGGCCCTGTCGACCACAGGCAAGGCCTTGAGG
                                                                                                                                                                                                                                                                1683 TGCTGAGCACGGGGTCAGGGCTGGAGGCACAGGCAGAGGGCAGAGGCTGG----
                                                                                    --ArgAspLeuGlyLeuLysG
                                                                                                                                                                                                                                                sAla-ArgGlyProSerAlaMet------ProAspProAlaGlnGlyProProS
                                                                                                                                    luGluLys------GlyLeuProLeuAlaLeuLeuAlaPro---LeuArgGlyAla-
                                                                                                                                                                                         ------AlaGluSerGlyGlyAlaAlaGlnProThrArgThr
                                                                                                                                                                                                                                                                                                    487 ysArgHisValAspSerGlnAlaProAsnThrGlyValProValAlaGlnProAlaLysS
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Location/Qualifiers
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JP 2002191363-A/13570.
Homo sapiens (human)
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ORGANISM
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ACCESSION
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                877 CAGCAGCTGCAGGCCGTGGTACCCCAGATAGACATGGAAGGGGATCGCAACATCTGGATC
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233
79
166
86
                                                                                                                                                                                      Matches:
Conservative:
Mismatches:
Indels:
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233
79
166
86
Primers for synthesising full-length cDNA and Patent: EP 1074617-A 15920 07-FEB-2001; Research Association for Biotechnology (JP) Location/Qualifiers
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Conservative:
Mismatches:
Indels:
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Organism="Homo sapiens"
/mol_type="unassigned DNA"
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        TITLE
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                                                                       FEATURES
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Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library

COMMENT

Commercial sections of

Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute

1176 1713 ATCCAGAAGCACCTGGAGAACTCATGCCATCGGCATCCACTCCGCTTCCGCCAGACAACATG 1296 1657 GAGGTGCCTCAATATGTGGGCATCCGGCTCCTGGTAGAGGCTTCACCATCAAGAAG--- 1713 261 512 -----ACAĠĊĄĊĄĠCAAĠĊŗĠGTGGGCACTAAGGCCCTGTCĠĄĊCACAGGĊĄĄGGC 1925 241 302 HisValGluProArgLysAsnSerPheGluLeuTyrGlyAlaAspPheValLeuGlyArg 321 359 GluProProProPheSerGlySerAspLeuCysValAlaGlyValSerValArgArgAla 397 398 ArgArgGlnValLeuProValCysAsnLeuLysAlaSerAlaSerLeuLeuAspAlaGln 417 457 477 497 LeuValThrAspTrpAsnProLeuThrIleTrpPheTyrLysGluSerTyrLeuArgPhe SerThrGlnArgPheSerLeuAspLysLeuAspSerAlaIleHisLeuCysAsnAsnAla LysTyrileGluThrProLeuLeuIleCysAspThrLysPheAspIleArgGlnTrpPhe 242 ValGlnLysTyrLeuLysAsnAspValGlyArgSerProLeuLeuProAlaHisAsnMet TrpThrSerThrArgPheGlnGluTyrLeuGlnArgGlnGlyArgGlyAlaValTrpGly AspPheArgProTrpLeulleGluIleAsnSerSerProThrMetHisProSerThrPro SerVallleTyrProSerMetLysLysAlalleAlaHisAlaMetLysValAlaGlnAsp 342 ValThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIleLysValAlaVal----418 ProteuLysAlaArgGlyProSerAlaMetProAspProAlaGlnGlyProProSerPro 438 AlaLeuGlnArgAspLeuGlyLeuLysGluGluLysGlyLeuProLeuAlaLeuLeuAla --AspProAsnGln---360 -----AspArgSerCysAspIleGlyAsnPheGluLeuLeuTrpArgGlnProValVal ProLeuArgGlyAlaAlaGluSerGlyGlyAlaAlaGlnProThrArgThrLysAlaAla GlyLysValGluLeuProAlaCysProCysArgHisValAspSerGlnAlaProAsnThr GlyValProValAlaGlnProAlaLysSerTrp----1713 ---166 1057 1117 222 1237 262 1297 282 322 182 202 378 1726 478 458 1825 498 1875 513 ઠે 셤 ઠે 셤 ò d ઠે 셤 ઠે g ઠે g ò ద ઠ g ò g ઠે ద ઠે 셤 셤 ઠે 셤 g ઠે δ ઠે 쉽 ò 셤 ò g ઠે

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RHFRPSLHYRAQLSPHVLAHQGVLRRQHSKLVGTKALSTTGKALSTTGKALTTTGRASEP
PPNLDPRVVAPSILKFRKAPALLCLRGPQLEVPCCLCPLKSEQFLAPVGRSRPKANSRP
construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnArglleThrSerValAsnProGlnThrAspIleAspGlyLeuArgAsnIleTrpIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCAGCTGCAGGCCGTGGTACCCCAGATAGACATGGAAGGGGATCGCAACATCTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysProArgAspGlnArgGluGluAlaGlySerSerAspLeuSerSerArgGlnAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549 AAAAAcccAGTGTTG-----GTGTCCCCAGAGTTTGTGAAGTCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValCysGlnAlaTyrLeuGlyGlnLeuGluHisGluAspIleAspThrSerAlaAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaSerSerIleLeuLysTrpValValSerHisGlnSerCysSerArgSerArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2326
233
79
166
86
                                                                                                    /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                      94. .>2326
/note="unnamed protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-2326)
                                                         Location/Qualifiers
                                                                                                                                                                                                                    codon_start=1
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1054.00
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41.4%
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Best Local Similarity:
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Pred. No.:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 ThrGinGlnTyrTyrSerLeuValHisGlyAspAlaPhelleSerAsnSerArgAsnTyr 113
                                                                                                                                                                                                                                                     154 ValCysMetAspArgValGluGluIleLeuGluLeuAlaAlaAlaAspHisProLeuSer 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyAlaAspPheValLeuGlyArgAspPheArgProTrpLeuIleGluIleAsnSerSer 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 GlnLeuValAspIleAlaCysLysValCysGlnAlaTyrLeuGlyGlnLeuGluHisGlu
                                                                                                                                                                                                                                                                                                                                     895 GACATCGACAAGGACCTGGAGGCCCGCTGTACCTCACCCCGAGGGCTGGTCCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 AspGlyLeuArgAsnIleTrpIleIleLysProAlaAlaLysSerArgGlyArgAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AlaIleHisLeuCysAsnAsnAlaValGlnLysTyrLeuLysAsnAspValGlyArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 GlnGlyArgGlyAlaValTrpGlySerValileTyrProSerMetLysLysAlaIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProThrMetHisProSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                            114 PheSerGlnCysGlnAlaLeuLeuAsnArglleThrSerValAsnProGlnThrAsplle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1195 AAGGACGGCAAGTGGGGGGGAAGTATATTGAGCGGCCCCTCCTCATCTTTGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrLysGluSerTyrLeuArgPheSerThrGlnArgPheSerLeuAspLysLeuAspSer
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                                                                        2553
220
69
151
81
                                                                        Length:
Matches:
Conservative:
                                                                                                                           Mismatches:
Indels:
                                                                                                                                                               Gaps:
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1020.00
55.5%
42.2%
35.7%
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Query Match:
DB:
                                                                                                       Percent Similarity:
                                                      Alignment Scores:
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Bequenced by AGOWA (Berlin/Germany) within the CDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp434B103) is available at the RZDD in Berlin.
Please contact the RZDD: Reseourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                  nomovuos/
Homo sapiens mRNA; cDNA DKF2p434B103 (from clone DKF2p434B103);
partial cds.
-----ACAGCACAGCAAGCTGGTGGGCACTAAGGCCCTGTCGACCACAGGCAAGGC 1925
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NSVHLCNNSIQKHERPLLPPDNWMSSQRFQAHLQRGAPNAWSTIVPGMX
AVIHALGYSQDTVQCRKASFELYGADSVPGEDPQPWILEINASPTWARCA
GVQADTLRVVIDRMLDRNCDTGAFELIYKQPVTTSPASTPRFSCLLPWYSDTRARSSD
                                                                                                         535
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (bases 1 to 2553)

Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

Direct Submission
Submitted (16-JUN-1999) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="festis"
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DH10B; sites NotI + SalI"
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                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                            HSM800637
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KEYWORDS
SOURCE
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Best Local Similarity: 42.2% Mismatches: 151 Query Match: 35.7% Indels: 81 DB: 6 Gaps: 12	US-10-635-977-2 (1-541) x AR339003 (1-3001)	Qy 54 GInLeuValAspIleAlaCysLysValCysGInAlaTyrLeuGlyGInLeuGluHisGlu 73 :::	Cy 74 AspileAspThrSerAlaAspAlaValGluAspLeuThrGluAlaGluTrpGluAspLeu 93	Db 1364 GATICGACAAAGAACTGAAGGCCCGGCTGTACCTCACCCCGGGGCTGGTCCTCTTC 1423 Qy 94 ThrGlnGlnTyrTyrSerLeuValHisGlyAspAlaPhelleSerAsnSerArgAsnTyr 113	Db 1424 CTCCAGCGCTACTACCAAGGGTCCACGAAGGGGCAGAACTCAGGCACCTCGACACTCAG 1483	1484 GTCCAGGGCTGTGAGACATCCTGCAGCAGCTGCAGGCCGTGGTACCCCAGATAGACATG 15	Qy 134 AspGlyLeuargAsnIleTrpIleIleIysProAlaAlaLysSerArgGlyArgAspIle 153 :::	154 ValCysMetAspArgValGluGluIleLeuGluLeuAlaAlaAlaAspHisProLeuSer 173	Db 1604 ATGTGCATGGACCACCTGGAGGAGATGCTGAAGCTGGTGAACGCAACCCCGTGGTGATG 1663 Qy 174 ArgaspasnLysTrpValValGlnLysTyrIleGluThrProLeuLeuIleCysAspThr 193	Db 1664 AAGGACGGCAAGTGGGTGCGGAAGTATATTGAGCGGCCCCTCCTCATCTTTGCCACC 1723 Ov 194 TwsPheasnleArdGlnTrDPheLeuValThrAspTrpAsnProLeuThrIleTrDPhe 213	1724 AAGTITGACCTCAGACAGTGGTTCCTGGTAACTGACTGGAACCCACTTACCGTGTGGTTC	Oy 214 TYTLYSGLUSerTYTLeuArgPheSerThrGlnArgPheSerLeuAspLeuAspSer 233	234	254 ProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArg	Db 1904 ccaccacacacacacacacacacacacacacacacaca
Qy 354 ThrileLysValAlaValAspArgSerCysAspIleGlyAsnPheGlu 369	370	Db 1795 CTCATCTATAAGCAGCCGTCACCACTTCCCCAGCCTCCACCAAGGC 1843 Oy 388 sValalaGlyValSerValArgArgAlaArgArgGlnValLeuProValCy8AsnLeuLy 408	1843	Qy 408 sAlaSerAlaSerLeuLeuAspAlaGlnProLeuLysAlaArgGlyProSerAlaMetPr 428	428 OA	448 ulysGlyjeuProLeuAlaLeuLeuAlaProLeuArgGlyAla 46	Db 1957 TACCCACGGCTAAGGTCTTCATTTCCCTCCCACCGAACCTTGATTTCAAGGTGGCACCCA 2016 Qy 463AlaGluSerGlyGlyAlaAlaGlnProThrArgThr 474	2017 GCATCCTGAAGCCAAGAAAGGTGGGCCTCGACCTGTGACTCACACCCAGTGGACAGTGCT	Qy 475LysAlaAlaGlyLysValGluLeuProAlaCysProCysAr 488	Qy 488 gHisValAspSerGlnAlaProAsnThrGlyValProValAlaGlnProAlaLysSerTr 508	S08 pAspproAsnGInLeuAsnAlaHisproLeuGluProValle			2260 A	AR339003

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Contact: nisc_mgc@nhgri.nin.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Caranite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
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AVITALQTSQTVQCRKASFELYGADPVFGBPFQPRLIEINASPTMARCS
GVQADTLRVVIDRRLDRNCDTGAFELLIKQPVTTSPASTPRPSCLLPMYSDTRARSSD
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CEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMK
                                                                                                                                                                                                                 Direct Submission
Submitted (15-JUL-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAM Plate: 4 Row: p Column: 10.
Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDMs sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                Center
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Clone_identification sequence tag: AGTCAG"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Cen
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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/db_xref="GeneID:26140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="TTLL3 protein"
/protein_id="AAH99735.1"
/db_xref="GI:71043428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GeneID:26140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-635-977-2 (1-541) x BC099735 (1-1769)
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56.9%
43.9%
35.1%
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Best Local Similarity:
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CONSRIM
TITLE
JOURNAL
CONSRIM
TITLE
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REFERENCE
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COMMENT
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Is bases 1 to 169)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collina, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Banchez, A., Whithny, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       2485
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC099735 1769 bp mRNA linear PRI 03-AUG-20
Homo sapiens tubulin tyrosine ligase-like family, member 3, mRNA
(cDNA clone MGC:120532 IMAGE:40025662), complete cds.
                    sValAlaGlyValSerValArgArgAlaArgArgGlnValLeuProValCysAsnLeuLy
                                                                                                                                                                                    ---- CCAGCTGCCTTCTCCCCATGTACTCCGACACCAGGGCCAGGTCCTCAGACGACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sAlaSerAlaSerLeuLeuAspAlaGlnProLeuLysAlaArgGlyProSerAlaMetPr
                                                                                                                                                                                                                                        428 oAspProAlaGlnGlyProProSerProAlaLeuGlnArgAspLeuGlyLeuLysGluGl
                                                                                                                                                                                                                                                                                                                                                       448 uLys------GlyLeuProLeuAlaLeuLeuAlaPro---LeuArgGlyAla----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2546 GAGCACGGGGTCAGGCTGGAGGCCACAGGCAGAGGCAGCTCCAGGCTGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522 uArgGlyLeuLysThrAlaGluGlyAlaLeuArgPro------ProProGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AlaGluSerGlyGlyAlaAlaGlnProThrArgThr-----
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BC099735.1 GI:71043427
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VERSION
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BC099735
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SOURCE
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Derge, J.G.,
men, C.M., Schuler, G.D.,
meer, C.F., Bhat, N.K.,
Wang, J., Hsieh, F.,
bin, G.M., Hong, L.,
coshiyuki, S.,
lo, N.A., Peters, G.J.,
lo, N.A., Peters, G.J.,
lichards, S.,
Hulyk, S.W.,
un, X., Glbbs, R.A.,
Rodrigues, S.,
Shevchenko, Y.,
Gareen, E.D.,
Schmutz, J., Myers, R.M.,
Schmutz, J., Myers, R.M.,
Schmutz, J., Myers, R.M.,
Schmutz, J., Myers, R.M., near PRI 03-AUG-2005 iily, member 3, mRNA ete cds. roAlaLeuGlnArgAsp 442 |||||| GTGCCTTG----- 1551 TACCCACGCTAAGGTC 1441 ----LeuLysalaarg 422 ||||||| GCATCCTGAAGCCAAGA 1501 -----CCC 1563 CCAAAGGCAAATTCAAG 1623 |||| ::: ------CATGAAGAG 1668 laAlaGlyLysValGlu 481 laProLeuArgGlyAla 462 roCysArgHisValAsp 491 393 SerValArgArgAlaArgGlnValLeuProValCysAsnLeuLysAlaSerAlaSer 412 brata; Euteleostomi; s; Catarrhini; of Health, Mammalian 30, USA 15,000 full-length CTTGTTGG 1701 ysserirp 508 16903 (2002) 8

662 193 722 213 782 233 842 253 902 273 962 293

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1323 CTCCCCATGTACTCCGACACCAGGCCAGGTCCTCAGACGACAGCAGCAGGTGGTGG 1382
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                                                                                                                                                                                                                                                                                                                                                                                                                       114 PheSerGlnCysGlnAlaLeuLeuAsnArgIleThrSerValAsnProGlnThrAspIle
                            GTCCAGCGCTGTGAGGACATCCTGCAGCAGCTGCAGGCCGTGGTACCCCAGATAGACATG
                                                                                          174 ArgAspAsnLysTrpValValGlnLysTyrIleGluThrProLeuLeuIleCysAspThr
                                                                                                                                                                                                                                                                                 LysPheAspIleArgGlnTrpPheLeuValThrAspTrpAsnProLeuThrIleTrpPhe
                                                                                                                                                                                                                                                                                                     ProLeuLeuProAlaHisAsnMetTrpThrSerThrArgPheGlnGluTyrLeuGlnArg
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                                                                      134 AspGlyLeuArgAsnileTrpileIleLysProAlaAlaLysSerArgGlyArgAspile
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                                                                                                                                                                                                                                             663 AAGGACGCCAAGTGGGTGGTGCAGAAGTATTGAGCGGCCCCTCCTCATCTTTGGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrileLysValAlaVal-----AspArgSerCysAspIleGlyAsnPheGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerValArgArgAlaArgArgGlnValLeuProValCy8AsnLeuLy8AlaSerAlaSer
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                                      483
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       Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
CDNA Library Pravayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granifard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAM Plate: 4 Row: o Column: 9.
Location/Qualifiers
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DGKWYVQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLD
NSVHLCNNSIQKHLENGCHRHPLLPPDNWWSSQRFQAHLQEMGAPNAMSTIIVPGKKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone Ilb="NIH MGC 283"
/note="Vector: pCR-Blunt II-TOPO with reversed insert;
Clone identification sequence tag: GAAGCCCCTGCTTCG"
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Matches:
Conservative:
Mismatches:
Indels:
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db_xref="GeneID:26140"
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cgapbs-r@mail.nih.gov
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LeuGlyLeuLysGluGluLysGlyLeuProLeuAlaLeuLeuAlaProLeuArgGlyAla 462

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Homo sapiens cDNA FLJ39917 fis, clone SPLEN2019405, highly similar to Homo sapiens HOTTL protein mRNA.

AK097236
AK097236.1 GI:21756925 oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                              174 ArgAspAsnLysTrpValValGlnLysTyrileGluThrProLeuLeuIleCysAspThr
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Research Association for Biotechnology (JP)
Location/Qualifiers
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Sequence 1766 from Patent EP1347046.
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AX834642.1 GI:39920777
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/db_xref="taxon:9606"
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Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kamehori, K., Takahashi-Fujii, A., Takeuchi, K., Atita, M., Imose, N., Musahino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Takura, S., Fukuzumi, Y., Pujimori, Y., Komiyama, M., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kababata, A., Hikiji, T., Kobatake, N., Naguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Nakajima, Y., Mata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shita, Y., Makajima, Y., Makajima, Y., Makaning, Y., Makaning, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shita, Y., Nakagawa, K., Okumura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakanura, R., Nakanura, R., Nakanura, R., Okumura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakanura, R., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length
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S 1809ai.T. and Yanamoto,J.

L Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazuaa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); CDNA ilbrary

Construction: Halix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsura,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai,Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Wurakawa,K., Kanehori,K.,
Takahashi-Pujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Magahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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/clone lib="SpleN2"
/note="cloning vector: pME18SFL3"
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                                                                                  94 ThrGlnGlnTyrTyrSerLeuValHisGlyAspAlaPheIleSerAsnSerArgAsnTyr
                                                                                                          1414 CTCCAGCGCTACTACCAAGTGGTCCACGAAGGGGCCAGCTCAGGCACCTCGACACTCAG
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                                                 13 GlnSerCysSerArgSerArgSerLysProArgAspGlnArgGluGluAlaGlySer
                                                                                                                  33 SerAspLeuSerSerArgGlnAspAlaGluAsnAlaGluAlaLysLeuArgGlyLeuPro
                                                                                                                                                                                          53 GlyGlnLeuValAspIleAlaCysLysValCysGlnAlaTyrLeuGlyGlnLeuGluHis
                                                                                                                                                                                                                                                         73 GluAspileAspThrSerAlaAspAlaValGluAspLeuThrGluAlaGluTrpGluAsp
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1. (bases 1 to 1832)

1. (bases 1 to 1832)

2. Smith, T.P., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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/protein_id="AAX46712.1"
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MAM 17-MAR-2005
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                family, member 3 (TTLL3),
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harhay,G.P., Sonstegard,T.S., Van Tassell,C.P., Clawson,M.
Heaton,M.P., Keele,J.W., Snelling,W.M., Weidmann,R.T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-MAR-2005) Molecular Genetic Research Unit, U.S. Meat Animal Research Center, P.O. Box 166, Spur 18D,
Center, NE 68933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gregory P. Harhay at harhay@email.marc.usda.gov.
Location/Qualifiers
   linear
1832 bp mRNA tubulin tyrosine ligase-like
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                                                                     BT021865.1 GI:61555425
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                                    mRNA, complete cds.
BT021865
                                                                                     FLI_CDNA.
Bos_taurus (cow)
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                  Bos taurus
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337 HisproSerThrProValThrAlaGlnLeuCysAlaGlnValGlnGluAspThrIleLys 356

317 PheValLeuGlyArgAspPheArgProTrpLeulleGlulleAsnSerSerProThrMet

938

1832 224 67 169 91

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.72e-41 960.50 53.1% 40.9% 33.7%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

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CGT 1057	Trp 372	::: TAC 1116	Val 392	TCC 1176	Ser 412	-CCC 1191	Gln 432	1229	uPr 452	 CCC 1286	453	CCC 1346	aAl 469	CTA 1406	lGl 481	TTT 1466	oVa 501	CTC 1526		
GCACCCTCCACGGCTGTCACCGCCAGGCTCTGTGCCGGTGTGCAGGCCGACACCCTGCGT		GTGGTCATCACTGGCGACTGGACCGCAC-TGTGACACGGGGGCCTTTGAGCTCATCTAC	ArgGlnProValValGluProProProPheSerGlySerAspLeuCysValAlaGlyVal	AAGCAGCCTGCCGTGGAGGTGCCCCAGTATGTGGGGTATCCGGCTTCTAGTAGAGGGCTCC	٠.	ACCATCAAGAAG	LeuLeuAspAlaGlnProLeuLysAlaArgGlyProSerAlaMetProAspProAlaGln	CTGGC-GATGAGTCACCGGCGGATGGCGTCCGCCCAGC	GlyProProSerProAla-LeuGlnArgAspLeuGlyLeuLysGluGluLysGlyLeuPr	CCTCCCTCACCTGCTGCCCCGAGGCTCTGGGGAAAGCAAAGGACTCAGGAAGCCC	obeu	: : : CATCCACAGCCCCTTACCACTTCCCAAGCCTCCACAGCAAGCCCCGGCTGCCTTCTCCCC	-AlaLeuLeuAlaProLeuArgGlyAlaAlaGluSerGlyGlyAlaAl	ATGTGCCCTGGCCCCAGGGCAGGTCCTCAGACTACAGCACGAAGCTGGTGGGCACTA	aGlnProThrArgThrLysAlaAlaGlyLysValGl	AGGCCCTGTCGACCACAGACAAGGCCTTGATGACTCTACCAACCGCCAAGGTTTTGATTT	uLeuProAlaCysProCysArgHisValAspSerGlnAlaProAsnThrGlyValProVa	CCCTCCCACCTAACCCTGAAGCTGGCACCCAACGCCTGAAAAAAGGCTC	lAlaGlnProAlaLysSerTrp 508	TTGCTCCCCAACGCCCTTCATGG 1548
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Search completed: April 4, 2006, 13:37:14 Job time: 7987 secs

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ORGANISM: Homo sapiens
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Matches 75; Conserv
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Sequence 26, Appl
Sequence 25994, A
Sequence 25993, A
Sequence 25992, A
Sequence 2, Appli
Sequence 9, Appli
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Sequence 12, Appl
Sequence 13, Appl
Sequence 56, Appl
Sequence 2408, Appl
Sequence 2408, Appl
Sequence 5799, Appl
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2871, Ap
10, Appl
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Sequence 67, Appl
Sequence 8, Appli
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                                                                     4, 2006, 12:59:01 ; Search time 5.39777 Seconds (without alignments) 1364.812 Million cell updates/sec
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Sequence 65,
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2: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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8: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-096-568A-25994

US-11-096-568A-25993

US-11-096-568A-25993

US-11-096-185-2

US-11-095-185-2

US-11-167-831-14

US-10-793-626-198

US-10-793-626-198

US-11-167-831-13

US-11-167-831-13

US-11-167-831-13

US-11-167-831-13

US-11-167-831-13

US-11-167-831-13

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Maximum Match 100%
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Sequence 5676, Ap
Sequence 2812; Ap
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Sequence 878, App
Sequence 879, App
Sequence 877, App
Sequence 2209, Ap
Sequence 2209, Ap
Sequence 544, App
Sequence 544, App
Sequence 544, App
Sequence 544, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
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Sequence 300, App
Sequence 32308, A
Sequence 399, App
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Sequence 399, App
Sequence 16, Appl
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US-10-995-561-878

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US-11-087-099-2209

US-11-087-099-9341

US-11-089-686-10927

US-11-098-686-10927

US-11-098-686-10927

US-11-098-686-10927

US-11-098-686-10927

US-11-098-688-3230

US-11-096-568A-32309

US-11-172-740-399

US-11-172-740-399

US-11-1096-568A-32308

US-11-1096-568A-32308

US-11-1096-568A-32308

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29.8%; Pred. No. 6.3e-20;
ive 45; Mismatches 86
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APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: STSHKA, MCHUNI
APPLICANT: OTSHKA, MCTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-03-07
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PAECHTIN VET. 2.1
SSOFTWARE: PAECHTIN VET. 2.1
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Publication No. US20060029945A1
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHI, SHIZUKO
APPLICANT: ISHI, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: YAMAMOTO, TUKO
APPLICANT: YOSUKA, KAORU
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IRIE, RYOTARO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 IWIIKPAAKSRGRDIVCMDRVEEILELAA----ADHPLSRDNKW-----VVQKYIETP
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352 ----KSPLYMLLKEHTVWSMEHLNRYISDTFWKARGLAKDW---VFTTLK 394
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367 FELFGFDILIDDNLKPWLLEVNYSPALTLDCSTDV 401
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FITLE OF INVENTION: Novel full length CDNA
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: UP 2001-379298
PRIOR FILING DATE: 2001-11-05
                                                                                                                                                           ; Sequence 3621, Application US/11072512; Publication No. US20060029945A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/11167856 Publication No. US20050268352A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wurtele, Eve S
Oliver, David J
Behal, Robert
Schnable, Patrick S
Ke, Jinshan
Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
                                                                                                                                                                                                                                                                                                                                                         WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                 APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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APPLICANT: Wurtele, Eve S
APPLICANT: Oliver, David J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAGAHARI, KENJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-072-512-3621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-167-856-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 G-----CKWTLSRFFSYLRS------WDVDDLLLWKKIHRMVILTILAIAPSVPFAANC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : || : || || : | : | : | : | | | : : | | | : : | | | : : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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                                                                                                                                                                                                                                         KNSFELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVA-----VD 228
                                                                                                                                                                                                                                                                           |: |||||| :: :| :||:||:||: |: 317 KHCFELYGYDILIDQDLKPWLLEVNASPSLTASSQEDYELKTCLLEDTLHVVDMEARLTG 376
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                                                                                                                                                                      --TSPDYHPKKGCKWTLQRFRQYLASKHGPEAV--ETLFRDIDNIFVKSLQSVQKVIISD 316
                                                                                                         121 SPLLPAHN-----MWISTRFQEYL-QRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPR 174
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   223 RKFDLRVYVLVMS------VFAECLLWSGHRR------QDVHLTNVAVQK--
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APPLICANT: MASUHO, YASUHIKO
TITLE OPE INVENTION: NOVAL Hull length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR SELING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HOO, YUKI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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NAGAI, KEIICHI
IRIE, RYOTARO
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Best Local Similarity
Matches 68; Conserv
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US-11-072-512-3371
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LENGTH: 592
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APPLICANT:
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Sequence 25933, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION Therby
TITLE OF INVENTION THERPY
TITLE OF INVENTION THERPY
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 25993
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| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
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| TITLE OF INVENTION: THERPER OF SEQ. ID NOS: 34471
| SEQ. ID NOS: 34471
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--GKK---YVMEEA 140
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                            168 OD-----HVEPRK-----NSFELYGADFVLGRDFRPWL 195
                                                                                                                                                                                                   168 OD-----HVEPRK-----NSFELYGADFVLGRDFRPWL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1)...(470)
; OTHER HOPRMATION: Ceres Seq. ID no. 13496424
US-11-096-568A-25993
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i LOCATION: (1)...(517)
cother information: Ceres Seq. ID no. 13496423
US-11-096-5688-25992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays subsp. mays
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                                : : |: ||
98 RVMLRQLRQAAGR----
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US-11-096-568A-25993
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US-11-096-568A-25992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 470
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US-11-096-568A-25994

i Sequence 25994, Application US/11096568A

i Sequence 25994, Application No. US20060046240A1

i GENERAL INFORMATION:
    APPLICANT: Alexandrov, Nickolai et al.
    A
APPLICANT: Lutziger, Isabelle
APPLICANT: Wen, Tsui-Jung
TILLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TILLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and
TITLE OF INVENTION: Accept Ca. Levels in Plants
FILE REFRENCE: P2194USDIV-2
CURRENT APPLICATION NUMBER: US 11/167,856
CURRENT FILING DATE: 2005-6-27
PRIOR APPLICATION NUMBER: US 09/234,865
PRIOR PILING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-26
PRIOR PELING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 38
NUMBER OF SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 PLIGAIAAGNTVLLK-----SELSPNASAFLAKTIPAYLDTKAIKVIEGGPDVATIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 ----WGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFELYG-----ADFVL-GRDFRPWLIE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LQHQWDKIFFTGSPKIGRIIMAAAAQHLTP--VTLELGGKSCISVDYVLIEKSFAPTLID 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 DIKEDIRQWFLVIDWNPL----TIMFYKESYLR-----FSTQRFSLDKLDSAIHLCNNAV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 Q---KYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 NKWVVQKYIETPLLICDTKFDI-----RQWFLVTDWN-PLTIWFYKESYLRFSTQRFSLD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.1%; Score 79.5; DB 7; Length 433; Best Local Similarity 22.5%; Pred. No. 2.9; Matches 42; Conservative 25; Mismatches 69; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 6.1%; Score 79; DB 7; Length 462; l Similarity 26.1%; Pred. No. 3.6; 42; Conservative 23; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
i LOCATION: (1)..(462)
correr INFORMATION: Ceres Seq. ID no. 13496425
US-11-096-5688-25994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis Thaliana
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ORGANISM: Zea mays subsp. mays
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239 M-LKPTI 244
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Best Local Similarity
Matches 42; Conserva
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US-11-167-831-14

Sequence 14, Application US/11167831

Publication No. US20060062805A1

Sequence 14, Application US/11167831

Publication No. US20060062805A1

GENERAL INFORMATION:
APPLICANT: ZHANG, YANJIN

TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
FILE REFERENCE: 8199-0006-55XCIP WO

CURRENT PAPLICATION NUMBER: US/11/167,831

CURRENT PILING DATE: 2005-06-28

PRIOR PAPLICATION NUMBER: US/09/601,326

PRIOR PAPLICATION NUMBER: ECT/US99/02630

PRIOR APPLICATION NUMBER: US 09/019,793

PRIOR PLILING DATE: 1999-04-19

PRIOR PLILING DATE: 1998-06-01

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 OGRGAVWGSVIYP-----SMKKAIAHAMKVAQDHVE------PRKNSFELYGADFV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSTQRFSLDKLDSAIHLCNNAVQKY-LKNDVGRSPLLPAHNMWT-----STRFQEYLQR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 WVVQKYIETPLLI------CDTKFDIRQWFLVTDW------NPLTIWFYKESYLR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 WMLSRSSWCPLLISLYFWPFCLASPSPVGWWSFASDWFAPRYSVRALPFTLSNYRRSYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73; Indels 100;
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                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Porcine reproductive and respiratory syndrome virus US-11-167-831-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
6.0%; Score 78; DB 7; Length 256;
Best Local Similarity 18.8%; Pred. No. 2.1;
Matches 48; Conservative 34; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 IVYNSTLNQVFAIFPTPGSRPKLHDFQQWLIAVHSS-
PRIOR APPLICATION NUMBER: US 08/301,435
PRIOR FILING DATE: 1994-09-01
PRIOR APPLICATION NUMBER: US 08/131,625
PRIOR PLILING DATE: 1993-10-05
PRIOR PLILING DATE: 1993-10-05
PRIOR PLILING DATE: 1992-10-30
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver. 2.0
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220 SVAASCTL--FVVLW 232
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SEQ ID NO 14
LENGTH: 256
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LENGTH: 256
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Sequence 2, Application US/11085185
Publication No. US20050287634A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 4600-0110PUS1
CURRENT APPLICATION NUMBER: US/11/085,185
CURRENT PILING DATE: 2005-03-22
PRIOR APPLICATION NUMBER: US 2004-188849
PRIOR PELLOR DOWNER: 2004-06-25
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 2
LENGTH: 549
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Sequence 9, Application US/11167831

Publication No. US2060062805A1

GENERAL INFORMATION:
APPLICANT: PAUL DR, PREM S

APPLICANT: ZHANG, YANJIN

TILLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
FILER ERFERRENCE: 8199-0005-55XCIP WO

CURRENT APPLICATION NUMBER: US/10/428,826

PRIOR APPLICATION NUMBER: US/10/428,826

PRIOR APPLICATION NUMBER: US/09/601,326

PRIOR FILING DATE: 2003-05-05

PRIOR PLING DATE: 1999-005

PRIOR PLING DATE: 1999-019

PRIOR PLING DATE: 1999-005

PRIOR FLING DATE: 1999-005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 YLRFSTQRFSLDKLDSAIHLCN---NAVQKYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQ 142
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                                                                                                                                               111 Q---KYLKNDVGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVA 167
                 DIKFDIRQWFLVTDWNPL----TIWFYKESYLR----FSTQRFSLDKLDSAIHLCNNAV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 VEEILELAAADHPLSRDNKWVVQKY-IETPLLICDTKFDIRQWFLVTDWNPLTIWFYKES 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 GRCAVW-----GSVIY-----PSMKKAIAHA------MKVAQDHVEPRKNSF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAAFSDRPRFAVGKYTAYDCSGLLWAPPEPYLRQARRICATELFSATRLESFEHIRDEEV
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----TVRLRDYLQMLALGVISRIVL---GKK---YVMEBA
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                                                                                                                                                                                                                                                                                168 QD-----HVEPRK-----NSFELYGADFVLGRDFRPWL 195
                                                                                                                                                                                                                                                                                                                  153 RVMLRQLRQAAGR-----
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US-11-085-185-2
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US-09-810-501-67
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                                                                                                                                                                                                                                            142 OGRGAVWGSVIYP-----SMKKAIAHAMKVAQDHVE------PRKNSFELYGADFV 186
                                                                                                                                                                                                                                                                       122 AGQ-AAWKQVVSEATLSRISSLDVVAHFQHLAAIEAETCKYLASRLPMLHNLRWIGSNVT 180
                                                                                                                                                                                                -----RDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKV 225
                                                                                                                                                                                                                                                                                                                                                        ----IFS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 DWN----PLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 MWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFE-LYGADFVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03104
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
                                                                                                                                   18 WMLSRSSWCPLLISLYFWPFCLASPSPVGWWSFASDWFAPRYSVRALPFTLSNYRRSYBA
                                                                                                    46 WVVQKYIETPLLI------CDTKFDIRQWFLVTDW-------NPLTIWFYKESYLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
US-10-793-626-198
                                                                      73; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                    DB 7; Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.0%; Score 78; DB 6; Length 667; Best Local Similarity 24.0%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Indels
                                                                                                                                                                                                                                                                                                                                       Score 78; DB 7; Pred. No. 2.1; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 198, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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Publication No. US2006002928A1
GENERAL INFORMATION:
APPLICANT: PAUL, PREM S.
                                  Query Match
Best Local Similarity 18.8%;
Matches 48; Conservative 3.
                                                                                                                                                                                                                                                                                                                                                                                     226 AVDRSCDIGNFELLW 240
                                                                                                                                                                                                                                                                                                                                                                                                                       220 SVAASČTL--FVVĽW 232
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                187 LG-----
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US-11-167-831-14
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US-09-810-501-67
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TITLE OF INVENTION: A POLYNUCLEIC ACID ISOLATED FROM A
PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRS
A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE
PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
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APPLICATION NUMBER: US/09/810,501
FILING DATE: 12-Mar-2001
CLASSIFICATION DATA:

PRIOR APPLICATION TOWNER: 08/301,435
FILING DATE: UNKNOWN>
APPLICATION NUMBER: 08/301,435
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 08/131,625
FILING DATE: COCT-1993
ATTORNEY/AGENT INFORMATION:

NAME: Lavalleye, Jean-Paul M.P.

REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 4625-021-55X CIP
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
MENG, XIANG-JIN
HALBUR, PATRICK G.
MOROZOV, IGOR
LUM, MELISSA A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 67:
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220 SVAASCTL--FVVLW 232
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STATE: Virginia
COUNTRY: U.S.A.
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226 AVDRSCDIGNFELLW 240
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220 SVAASCTL--FVVLW 232
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APPLICANT: ZHANG, YANNINS

APPLICANT: ZHANG, YANNINS

TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE

TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)

FILE REFERENCE: 8199-0005-55XCIP WO

CURRENT APPLICATION NUMBER: US/11/167,831

CURRENT PILING DATE: 2005-06-28

PRIOR APPLICATION NUMBER: US/09/601,326

PRIOR APPLICATION NUMBER: US/09/019,736

PRIOR APPLICATION NUMBER: US 09/019,736

PRIOR FILING DATE: 1999-04-19

PRIOR PILING DATE: 1999-04-19

PRIOR APPLICATION NUMBER: US 08/019,733

PRIOR APPLICATION NUMBER: US 08/019,733

PRIOR APPLICATION NUMBER: US 08/019,733

PRIOR APPLICATION NUMBER: US 08/31,435

PRIOR FILING DATE: 1994-09-01

PRIOR FILING DATE: 1991-09-01

PRIOR FILING DATE: 1991-09-01

PRIOR FILING DATE: 1991-09-01

PRIOR FILING DATE: US 08/131,625

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SGEQUENCE 11, Application US/11167831
SGEQUENCE 11. Application No. US20060062805A1
Publication No. US20060062805A1
GGENERAL INFORMATION:
APPLICANT: PAUL DR. PREM S
TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
FILE REFERENCE: 8199-0005-55XCIP WO
CURRENT APPLICATION NUMBER: 2001-5005-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74; Indels 100; Gaps
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Sequence 12, Application US/11167831

Sequence 12, Application US/11167831

Bublication No. US20060062805A1

GENERAL INFORMATION:
APPLICANT: APUL DK. PREM
TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
TITLE OF INVENTION: REPRODUCTIVE AND REPIRATORY SYNDROME VIRUS (PPRSV)
CURRENT FILING DATE: 2003-506-28

PRIOR APPLICATION NUMBER: US/09/601,326

PRIOR PELING DATE: 2000-09-25

PRIOR PELING DATE: 1999-04-19

PRIOR PELING DATE: 1999-04-19

PRIOR PELING DATE: 1999-02-06

PRIOR PELING DATE: 1999-00-01
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5.9%; Score 77; DB 7; Length 256;
Best Local Similarity 18.4%; Pred. No. 2.7;
Matches 47; Conservative 35; Mismatches 73; Indels
PRIOR APPLICATION NUMBER: US/10/428,826
PRIOR FILING DATE: 2003-05-05
PRIOR PLING DATE: 2003-05-05
PRIOR PLING DATE: 2003-05-05
PRIOR PLING DATE: 2000-09-25
PRIOR PLING DATE: 1999-04-19
PRIOR PLING DATE: 1999-04-19
PRIOR PLING DATE: 1996-02-06
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PRIOR PLING DATE: 1993-10-05
PRIOR PLING DATE: 1993-10-30
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89 FSTORFSLDKLDSAIHLCNNAVQKY-LKNDVGRSPLLPAHNMWT-----STRFQEYLQR 141
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78 FLSQ-------CQVDIPTWGTKHPLG---MFWHHKVSTLIDEMVSRRMYRIMEK 121
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                                                                                                                                                                                                                                                                                                                 46 WVVQKYIETPLLICD-----TKFDIRQWFLVTDW------NPLTIWFYKESYLR 88
                                                                                                                                                                                                                                                                                                                                           Query Match 5.9%; Score 76; DB 7; Length 256;
Best Local Similarity 18.4%; Pred. No. 3.4;
Matches 47; Conservative 34; Mismatches 74; Indels 100; Gaps
PRIOR APPLICATION NUMBER: US 08/131,625
PRIOR FILING DATE: 1993-10-05
PRIOR FILING DATE: 1993-10-05
PRIOR FILING DATE: 1993-10-30
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 256
TYPE: PRT
ORGANISM: Porcine reproductive and respiratory syndrome virus
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181 IVYNSTSEQVFAIFPTPGSRPKLHDFQQWLIAVHSS-
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220 SVAASCTL--FVVLW 232
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US-11-167-831-12
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Sequence 4, Application US/10635977
Publication No. US20040171131A1
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Sequence 4, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
RIOR APPLICATION NUMBER: US. 60/394,725
PRIOR APPLICATION NUMBER: US. 60/394,725
RIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4.2
                                 Sequence 7680, Ap Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 21, Appl Sequence 38213, A Sequence 38213, A Sequence 252294, Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 118, Appli Sequence 118, Appli Sequence 118, Appli
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US-11-097-143-7680
US-10-615-659-21
US-10-615-659-21
US-10-635-977-22
US-10-635-977-22
US-10-635-977-22
US-10-635-977-22
US-10-635-977-22
US-10-104-047-3371
US-11-097-143-21303
US-10-615-659-6
US-10-615-659-6
US-10-615-659-6
US-10-210-118
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US-10-108-26A-2495
US-11-08-26A-2495
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Sequence 13, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: D0283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT APPLICATION NUMBER: US. 60/394,725
PRIOR APPLICATION NUMBER: U.S. 60/394,725
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
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Publication No. US20040171131A1

Publication No. US20040171131A1

APPLICANT: Bristol-Myers Squibb Company

ITILE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: DO283A CIP

CURRENT APPLICATION NUMBER: US/10/635,977
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        SPLLPAHNWWTSTRFQEYLQRGCRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180
                                                                                   253 SPLLPAHNWHTSTRFQEYLQRGGRGAVWGSVIYPSWKKAIAHAMKVAQDHVEPRKNSFEL 312
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100.0%; Pred. No. 9.5e-129;
tive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REPERENCE: DO23A3 CIP
CURRENT APPLICATION NUMBER: US/10/635,977
CURRENT PILING DATE: 2003-08-07
PRIOR FILING DATE: 2003-07-09
PRIOR FILING DATE: 2003-07-09
PRIOR FILING DATE: 2003-07-09
REIOR FILING DATE: 2003-07-09
SEQ ID NO: 103
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 4
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REPERENCE: D0283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: U.S. 60/394,725
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.2
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US-10-615-659-2
Sequence 2, Application US/10615659
Publication No. US20040157234A1
GENERAL INFORMATION:
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US-10-615-659-2
                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-10-635-977-4
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1.FNGTH: 541
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Sequence 14, Application US/10635977

| Publication No. US2004017131A1
| Publication No. US2004017131A1
| GENERAL INFORMATION:
| APPLICANT: Bristol-Myers Squibb Company
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
| TITLE OF INVENTION: POLSA CIP
| CURRENT APPLICATION NUMBER: U.S. 60/394,725
| PRIOR PELLING DATE: 2002-07-09
| PRIOR PAPLICATION NUMBER: U.S. 60/394,725
| PRIOR PAPLICATION NUMBER: U.S. 10/615,659
| NUMBER: DATE: 2003-07-09
| NUMBER: DATE: PATENTING DATE: 2003-07-09
| NUMBER: PATENTING DATE: 2003-07-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/10615659
Publication Vo. US2040157234A1
GENERAL INFORMATION:
THUEL OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TROSINE-LIGASE-LIKE PROTEIN, BGS42
TITLE OF INVENTION: US/10/615,659
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT APPLICATION NUMBER: US. 60/394,725
PRIOR APPLICATION NUMBER: US. 60/394,725
PRIOR FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
                  121 SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180
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Best Local Similarity 100.0%; Pred. No. 1.4e-123;
Matches 233; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Publication No. US20040171131A1

GENERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42

CURRENT APPLICATION NUMBER: US/10/635,977

CURRENT FILING DATE: 2003-09-07

PRIOR FILING DATE: 2002-07-09

PRIOR FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SSOFTWARE: PATCHTION NUMBER: U.S.10/615,659

SEQ ID NO 13

LENGTH: 541
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                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1299; DB 4;
100.0%; Pred. No. 9.5e-129;
tive 0; Mismatches 0;
CURRENT FILING DATE: 2003-08-07

PRIOR APPLICATION NUMBER: U.S. 60/394,725

PRIOR FILING DATE: 2002-07-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Patentin version 3.2

LENGTH: 541
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Best Local Similarity 100.
Matches 242; Conservative
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US-10-635-977-2
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US-10-635-977-13
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Publication No. US20040157234A1
GENERAL INFORMATION:
APPLICANT: Bristol—Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
TITLE OF INVENTION: TYROSINE-LIGASE-LIKE PROTEIN, BGS42
FILE REFERENCE: D0283 NP
CURRENT APPLICATION NUMBER: US/10/615,659
CURRENT PILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: U.S. 60/394,725
PRIOR FILING DATE: 2002-07-09
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                                                                                  Length 293;
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                                                                                                                 Indels
                                                                              Query Match 96.0%; Score 1247; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e-123;
Matches 233; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 7
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Best Local Similarity 61.8*
Matches 152; Conservative
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-635-977-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-615-659-7
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ELIYKQ 306
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                                                                                  Query Match
Best Local Similarity
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RESULT

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RESULT 11
US-10-756-149-5267
US-10-756-149-5267
; Sequence 5267, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF METASTATIC CANCER,
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; TITLE OF INVENTION: METHOD SOF SCREENING FOR MODULATORS OF METASTATIC CANCER
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PALENTIN VERSION 3.2
; SEQ ID NO 5267
: LENGTH: 352
Sequence 7, Application US/10635977

Publication No. US20040171131A1

Publication No. US20040171131A1

ABRIERAL INFORMATION:

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN

TITLE OF INVENTION: TROSINE-LIGASE-LIKE PROTEIN, BGS42

TITLE OF INVENTION: TROSINE-LIGASE-LIKE PROTEIN, BGS42

FILE REFERENCE: D0283A CIP

CURRENT APPLICATION NUMBER: US.10/615,977

CURRENT FILING DATE: 2003-08-07

PRIOR FILING DATE: 2002-09

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 103

NUMBER OF SEQ ID NOS: 103

SOFTWARE: Patentin version 3.2
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65.4%; Score 850; DB 4; Length 352;
Best Local Similarity 61.8%; Pred. No. 2.6e-81;
Matches 152; Conservative 41; Mismatches 49; Indels
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61.8%; Pred. No. 2.6e-81;
iive 41; Mismatches 49;
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ORGANISM: Homo sapiens
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ELIYKQ 306
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LAL, Preeti
YAO, Monique G.
BANDMAN, Olga
BURFORD, Neil
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318 ELIYKO 323
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LENGTH: 362
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APPLICANT:
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                                                                TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
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Publication No. US20020039764A1
GENERAL INFORMATION:
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US-10-102-806-617
; Sequence 617, Application US/10102806
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ELIYKQ 306
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ELIYKQ 323
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, LOCATION: (307)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-617
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PIC1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT PILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
NUMBER OF SEQ ID NOS: 846
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APPLICANT: KEARNEY, Liam
APPLICANT: KEARNEY, Liam
APPLICANT: POLICKY, Jennifer L.
TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
FILE REFERENCE: PF-0772 USN
CURRENT APPLICATION NUMBER: US/10/275,595A
CURRENT FILING DATE: 2003-06-13
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APPLICANT: TANG, Y. TOM
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Dyung Aina M.
APPLICANT: HULMAN, Jennifer L.
APPLICANT: AZIMZAI, Yalda
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GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560AIeI full length cDNA; FILE REFRENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 4209
LENGTH: 326
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.4%; Score 850; DB 4; Length 488; Best Local Similarity 61.8%; Pred. No. 4.1e-81; Matches 152; Conservative 41; Mismatches 49; Indels
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OTHER INFORMATION: Incyte ID No: 2156553CD1
PRIOR APPLICATION NUMBER: US 60/201,960
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/202,729
PRIOR PILING DATE: 2000-05-08
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
NUMBER: OF SEQ ID NOS: 68
SOFTWARE: PERL PROGRAM
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Best Local Similarity 61.89
Matches 152; Conservative
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US-10-108-260A-4209
                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Db 121 TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKOLLDNSJQKHLENSCHR 180

Qy 121 SPLLPAHNWHTSTRFQEYLQRGRGAVWGSVIYPSWKKALAHAMKVAQDHVEPRKNSFEL 180

Db 181 HPLLPPDNWMSSQRFQAHLQEMGAPNAWSTIIVPGMKDAVHALQTSQDTVQCRKASFEL 240

Qy 181 YGADFVLGRDFRPWLIEINSSFTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF 236

Qy 237 ELLWRQ 242

Db 301 ELIYKQ 306

Search completed: April 4, 2006, 12:58:00

Job time: 34:8606 secs
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US-10-104-047-3371
Sequence 3371, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
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REKRVGGFDLMW 388
 TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3658
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Sequence 45703, A
Sequence 46703, A
Sequence 62411, Ap
Sequence 146787, A
Sequence 14673, A
Sequence 31, Appl
Sequence 62317, A
Sequence 20939, A
Sequence 20939, A
Sequence 12140, A
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1 IDGLRNIWIIKPAAKSRGRD.....IKVAVDRSCDIGNFELLWRQ 242
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6_COMB.pep:*

(cgn2_6/ptodata/1/iaa/H_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*

(cgn2_6/ptodata/1/iaa/RE COMB.pep:*

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US-10-104-047-3621

US-09-270-767-62411

US-09-270-767-467187

US-09-270-767-467187

US-09-270-767-46717

US-09-270-767-62317

US-09-270-767-62317

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US-09-270-767-62317

US-09-270-767-62317

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US-09-270-778-12140

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Maximum Match 100%
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Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REPERENCE: H1-A0105;
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR PELICATION NUMBER:
PRIOR PELICATION NUMBER:
SPRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3658
LENGTH: 439
US-09-113-750A-37
US-09-019-793A-9
US-09-019-793A-14
US-09-601-326-14
PCT-US95-09927-3
US-09-710-279-198
US-09-605-703B-808
US-09-605-703B-808
US-09-605-703B-808
US-09-605-703B-808
US-09-805-703B-808
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US-09-808-878-316-8
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29.8%; Pred. No. 3.8e-22;
iive 45; Mismatches 86
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US-08-301-435-67
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US-09-601-326-11
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Best Local Similarity 29.8
Matches 75; Conservative
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SEQ ID NO 3621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 G-----CKWTLSRFFSYLRS------WDVDDLLLWKKIHRWVLLTILAIAPSVPFAANC 366
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Sequence 46703, Application US/09270767

Sequence 46703, Application US/09270767

Sequence 46703, Application US/09270767

FRIEDRIAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

FILE REFERENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 46703

LENGTH: 561
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          TITLE OF INVENTION: NO. 6943241el full length cDNA FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 3371
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20.8%; Score 270; DB 2;
Best Local Similarity 31.6%; Pred. No. 7.7e-22;
Matches 68; Conservative 40; Mismatches 73;
APPLICANT: HELIX RESEARCH INSTITUTE
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US-09-270-767-46703
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                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 IWICKPTASNQCKGIFLLRNQEEVAALQAKTRSMEDDPIHHKTPFRGPQARVVQRYIQNP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 LLVDGRKFDVRSYLLIACTTPYMI-FFGHGYARLTLSLYDPHSSDLGGHLTNOFMQK--- 351
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Sequence 62411, Application US/09270767

Sequence 62411, Application US/09270767

Fatert No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 62411

LENGTH: 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.6%; Score 177; DB 2; Length 404; 28.2%; Pred. No. 1.9e-11; ive 27; Mismatches 65; Indels
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; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELLIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6942241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION UNMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%; Score 153.5; DB 2
35.6%; Pred. No. 4.9e-09;
tive 15; Mismatches 39
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US-09-270-767-46787
; Sequence 46787, Application US/09270767
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US-09-270-767-62411
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                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-10-104-047-3621
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Best Local Similarity
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95 -----SLDKLDSAIHLCNNAVQKYLKNDVGRSPLLPAHNWWTSTRFQ---EYLQRQGRG 145
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## Sequence 31, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Mansfield, Traci A. |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same |
| TITLE OF INVENTION: PROTEIN US/09/538,092 |
| CURRENT APPLICATION NUMBER: 60/127,352 |
| PRIOR PELICATION NUMBER: 60/127,352 |
| PRIOR PELICATION NUMBER: 60/127,352 |
| PRIOR PELICATION NUMBER: 60/178,965 |
| PRIOR PLING DATE: 2000-02-01 |
| NUMBER OF SEQ ID NOS: 1387 |
| SOFTWARE: CuraPatSeqFormatter Version 0.9 |
| SEQ ID NO 31 |
| LENGTH: 753 |
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ IN NOS: 62517
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 46577
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YBR094W
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23.6%; Pred. No. 8.6e-06;
tive 36; Mismatches 62.
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ORGANISM: Saccharomyces cerevisiae
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; ORGANISM: Drosophila melanogaster
US-09-270-767-46577
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Best Local Similarity
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Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Meinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 GLDNHWIIKPWNLARGLDTHITDNIKQIVRLPAT-----GPKIAQKYIBRPVLFSROE 457
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                                                                                   APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster CURRENT FILLS REFERENCE: File Reference: 7326-094
CURRENT PILLING NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLIC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ---DTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLD 100
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11.8%; Score 153.5; Best Local Similarity 35.6%; Pred. No. 1.3e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14603
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-767-46787
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LENGTH: 507
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US-09-538-092-31
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 0.060-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12140
LENGTH: 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 WVSLLTDPAVSGMARDVVLSDAMMGYLHFISGIP--TQGTRWL---YSSTPYKMATPPLS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -IROWFLVTDWN--PLTIWFYKESYLRFSTORFSLDKLDSAIHLCNNAVQKYLKNDVGRS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 PLLPAHNMWTST--RFQEYLQRQG-----RGAVWGSVIYPSMKKAIAHAMKVAQDH--V 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 STRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQ--DHVEPRKNSFELYGADFVLGR 189
                              557 IEBENBYFMSDRKGF---SSFKPLIDNGYIDAIKTKETVKKRKSRKSSTSAFNKDI---S 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 WI----IKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFD 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 607;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.7%; Score 87.5; DB Best Local Similarity 25.2%; Pred. No. 0.61; Matches 52; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E--PRKNSFELYGADFVLGRDFRPWL 195
                                                                                                                                                                                                                                           Sequence 12140, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION: APPLICANT: Gary Breton et. al
                                                                                              190 DFRPWLIEINSSPTMHPS 207
                                                                                                                        611 DFRQGLRRENNGESFPPT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12140
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STATE: none
COUNTRY: Switzerland
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US-09-489-039A-12140
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US-07-857-224B-33
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
REIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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                                                                                                     107 NNAVOKYLKNDVGRSPLLPA------HNWW---TSTRFQEYLQRQGR--GAVWGSVI 152
                                                                                                                                                                                                                                                                                                            Sequence 62117, Application US/09270767

Sequence 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                             109 HIVRTTIAAKEKDIVNILRSYRTH----NFFDLMRFDLFIDEDLKVFLMEANMSPNL 161
                                                                                                                                                                    153 Y-----PSMKKAIAHAMKVAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSPTM 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 DIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQWFLVTDW---NP
      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Score 102; DB 2; Best Local Similarity 43.8%; Pred. No. 0.00038; Matches 21; Conservative 10; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 91.5; DB 23.7%; Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20939, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Drosophila melanogaster US-09-270-767-62317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Conservative
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US-09-248-796A-20939
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Best Local Similarity
Matches 47; Conserv
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US-09-248-796A-20939
                                                                                                                                                                                                                                                                                                          US-09-270-767-62317
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103 IHLCNNAVQKYLKNDVGR-SPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIA 161
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Patent No. 6476213
GENERAL INFORMATION:
APPLICANT: Suerbaum, Sebastian
TITLE OF INVENTION: Cloning and Characterization Production
of Aflagellate Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.4%; Score 83; DB 2; Length 732; Best Local Similarity 24.5%; Pred. No. 2.6; Matches 51; Conservative 31; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
Dunner
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                 SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                 NAME: Meyers, Kenneth J.
RECISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0073-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,757A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/671,757A FILING DATE: 16-449-2001 CLASSIFICATION: «Unknown» ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 HAMKVAQ-----DHVEPRKNS-FELYG 182
            OPERATING SYSTEM: PC-DOS/MS-DÓS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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                                                                                                  FILING DATE: 16-Aug-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 732 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-671-757A-8
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Sequence 7, Application US/08671757A
Sequence 7, Application US/08671757A
Patent No. 6476213
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Suerbaum, Sebastian
TITLE OF INVENTION: Cloning and Characterization Production
of Aflagellate Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 6.4%; Score 83.5; DB 1; Length 268;
l Similarity 21.4%; Pred. No. 0.52;
54; Conservative 33; Mismatches 100; Indels 6:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEPHAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 37
PUBLICATION INFORMATION:
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
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                                                                                                         TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 268
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                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                protein
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MOLECULE TYPE:
DESCRIPTION: prot
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Best Local Similarity
Matches 54; Conserv
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103 IHLCNNAVQKYLKNDVGR-SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIA 161
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REFERENCE/DOCKET NUMBER: 02356.0073-00000
           TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 732 amino acids

TYPE: amino acids

TYPE: amino acid

STRANDEDNESS: single

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-671-757A-8
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1 IDGLRNIWIIKPAAKSRGRD.....IKVAVDRSCDIGNFELLWRQ 242
                                                                                    4, 2006, 12:43:06; Search time 36.6599 Seconds
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Q6bfh6
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          GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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Q4RMS HUMAN
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Q9RN1 HUMAN
Q9RV1 MOUSE
Q9ZZTO MOUSE
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Q9W91 DROME
Q7Q15 6 ANOCA
Q9VW91 DROME
Q9VW91 DROME
Q5HV1 DROME
Q5HV1 DROME
Q5HV1 DROME
Q5TW2 HUMAN
Q6TW2 HUMAN
Q6TW7 RAT
Q9D570 MOUSE
Q6GG8 HUMAN
Q64TW1 BICDI
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Q9D571 DROME
Q65TW1 BICDI
Q6BFH6 PARTE
Q6G119 DROME
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Maximum Match 100%
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homo sapien
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mus musculu
                                                                                                                                                                                                                                                                                                                                                           rattus norv
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drosophila
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 LICDTKFDIROWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 LICDTKFDIRQWFLVTDWNPLTIWFYKSYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKN
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AL022127; CAI42686.1; -; Genomic_DNA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0004844; P:protein modification; IEA.
InterPro; IPR004344; Tub_tyr_lygase.
Pfam; PF03133; TTL; 1.
NON_TER
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Q5JZ84;
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
OTTHUMPO0000028514 (Fragment).
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TTLLI HUMM.
TTLLI MOUSE
2 O54384 MOUSE
- PDI9 RAT
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                                                                                                         QOULUS HUMAN
QOUEZA HUMAN
QOEEF3 CERAE
QOEEF3 CERAE
QOEEF3 PONPY
TILLI HUMAN
                              Q8C125_MOUSE
Q8CFV5_MOUSE
Q8CHB8_MOUSE
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Best Local Similarity 98.4
Matches 242; Conservative
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ID QBCGV2_MOUSE PRELIMINARY;
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   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C5/BL/6J; IISSUB=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Indone and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                  01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-OT-2003 (TYEMBLrel. 25, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4930524K07 product:hypothetical Tubulin-tyrosine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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"Functional annotation of a full-length mouse cDNA collection.";
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                        Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
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                                                                                                                                                                                    Name=1700019P01Rik;
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Carralle-C57BL/62; TISSUE-Teetis;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Hangaki T., Hara A., Hashizume W., Hayatsu M., Hangaki T., Hara A., Hashizume W., Hayashida K., Hayatsu I., Hiraoka T., Hirozane T., Hayatsu I., Kilmi Y., Konno H., Kouda M., Koya S., Atoch H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Kaya I., Miyazaki R., Ohno M., Ohaaco N., Okazaki Y., Saito R., Saito H., Sakai C., Sakai K., Ohno M., Ohasuo N., Sano H., Saito R., Saito H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Saito H., Takau A., Shirada T., Takau A., Shiraki T., Sogabe Y., Tagami M., Agawa A., Takahashi F., Takaku A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Shibate (JUL-2011) to the EMBL/GenBank/DDBJ databases.

Brill, AKO29745; BAC26595.1; **, **mRNA*

Brill, MG:1922902; 1700019POIRik.

CG: G0:0016874; F:ligase activity; IEA.

GG: G0:0016844; F:ligase activity; IEA.

CO: G0:0016845; F:tubulin-tyrosine ligase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIXEN full-length enriched
library, clone:4933401B17 product:hypothetical Tubulin-tyrosine ligase
containing protein, full insert sequence.
Name=1700019P01Rik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNSIQRRLKNDKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 YGADFILGRDFKPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVVVDRKLDRNCDIGNF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Ligase.
SEQUENCE 518 AA; 59319 MW; 540C045659FACOD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1143; DB 2;
Pred. No. 5.4e-94;
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17; Mismatches
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Pfam; PF03133; TTL; 1.
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85.0%;
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QBCON7;
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209; Conservative
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                                                                                                                   NUCLEOTIDE SEQUENCE
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STRAIN-CSTBL/61; TISSUE-Testis;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
Thanalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hashizume W., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Haramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Ş., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Shinada A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tonaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 IDGIRNIWIIKPAAKSRGRDIVCMDRVENILSLVAADSQTTKDNKWVVQKYIETPMLIYD 395
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Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
Liu M., He F.;
"Functional prediction of the coding sequences of 50 new genes deduced
by analysis of cDNA clones from human fetal liver.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNSIQRRLKNDKER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
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                                                                                                                                                                                                                                                                                                                                                                                           Matches 209; Conservative 17; Mismatches
EMBL; AK030151; BAC26811.1; -; mRNA.
Ensembl; ENSMUSG0000022388; Mus musculus.
MGI; MGI:1922902; 1700019P01Rik.
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Name=TTLL3;
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Name-DKFZp686D076;

Name-DKFZp686D076;

Homo sapiens (Human)

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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EMBL, BK648175; CAH10554.1; -; mRNA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:006484; P:protein modification; IEA.
PF03133; TTL; 1.
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                                                                                                            M -> R (in dbSNP:2290305).
/FTId=VAR_020207.
I -> F (in Ref. 2).
; 49FD8E8118C7C20D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l protein.
352 AA; 40257 MW; 49FD8E9CAE1CB20D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 850; DB 2;
61.8%; Pred. No. 7.6e-68;
iive 41; Mismatches 49;
                                                                                                                                                                          65.4%; Score 850; DB 1;
61.8%; Pred. No. 7.6e-68;
tive 41; Mismatches 49;
           EMBL; AF078842; AAF23353.1; -; mRNA.
PIR; T12515; T12515.
Ensembl; ENSG00000156983; Homo sapiens.
                                               HGNC; HGNC:24483; TTLL3.
InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
EMBL; AL096725; CAB46375.1; -; mRNA
                                                                                                                                                   40356 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cervix;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OGAWA3_HUMAN PRELIMINARY;
                                                                                                                                                                                       Best Local Similarity 61.89
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                  293
                                                                                     Ligase; Polymorphism.
DOMAIN 1
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                                                                                                                                     67
352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLWRQ 242
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Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELIYKÖ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                               290
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                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                              61
                                                                                                              VARIANT
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6AWA3;
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TISSUB-PCR rescued clones;

NUCLEOTIDE SEQUENCE.

TISSUB-PCR rescued clones;

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ALE                                                                                                                                                                                                                                                                                                                    241 YGADFVFGEDFQPWLIEINASPTMAPSTAVTARLCAGVQADTLRVVIDRMLDRNCDTGAF 300
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                           181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                   61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                       121 SPLLPAHNWWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BC098361, AAH98361.1; -; mRNA.
EMBL, BC099735, AAH99735.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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352 AA; 40381 MW; 49EF0C1118C7DD12 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Hypothetical protein (TTLL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rescued clones;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4KMS8_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sednences.
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ELIYKQ 306
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SEQUENCE 35
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                              1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                       121 SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                                                                                       181 HPLLPPDNWWSSQRFQAHLQEMGAPNAWSTIIVPGMKDAVIHALQTSQDTVQCRKASFEL
                                                                                                                                          YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                     TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                   Gaps
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                     4;
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  Length 352;
                   49; Indels
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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65.4%; Score 850; DB 2;
61.8%; Pred. No. 7.6e-68;
ive 41; Mismatches 49;
                                                                                                                                                                                                                                         434 AA
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created 01-0CT-2002 (TrEMBLrel. 22, Last sel 13-SEP-2005 (TrEMBLrel. 31, Last an Hypothetical protein DKFZp586B0320. Name-DKFZp586B0320;
                                                                                                                                                                                                                                       QBNDN8 HUMAN PRELIMINARY;
Q8NDN8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse cDNA sequences."
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                   Conservative
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         Similarity
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                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Uterus;
                  152;
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Query Match
Best Local 3
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                 Matches
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RC TISSUB-Thyroid gland;

RR VILEDOILDS SEQUENCE.

RA OFA T., SUZUKİ Y., NISHIKAWA T., OLGUKİTLE R.,

RA OFA T., SUZUKİ Y., NISHIKAWA T., OLGUKİT T., SUGİYYAMA T., TITLE R.,

RA GAT., SUZUKİ Y., NISHIKAWA T., OLGUKİT T., TANAKLA H.,

RA SEKINE M., ODAYASHI M., NISHI T., SHIDBABATA T., TANAKAMURA Y.,

RA SAMAMOKO Ö.T., SAİLO K., KAWAİ Y., ISONO Y., NAKAMURA Y.,

RA MARAMATI K., MUZAKAMİ K., YSONOİT T., FULUYA T., KİKAWA E.,

RA SHITATORI A., SUGO H., HOSOIRI T., KAKU Y., KOĞAİRA H., KONDÖ H.,

RA SHITATORI A., SUĞO H., HOSOIRI T., YONOĞI T., FULUYA T., KİKAWA E.,

RA SHITATORI A., NINOMIYA K., ISHİDBABİ T., YAMASHILA H., MUZAKAWA K.,

RA YAMAZAKİ M., NINOMIYA K., ISHİDBABİ T., YAMASHILA H., MUZAKAWA K.,

RA İSHİĞA S., ONO Y., TAKİĞUÇDİ S., WATADIADA S., YOSIĞA M., HOLULA T.,

RA NOMIZA Y., TOĞIYA S., KOMAİ F., HARA R., TAKBUCHİ K., ALTEA M.,

RA NOMIZA S., KOMAİ F., HARA R., TAKBUCHİ K., ALTEA M.,

RA YOSHİKAWA Y., MATSUNAMİ H., ÖĞDİMA A., SABBAİNA Y., SALOK S.,

RA NAKAĞARA S., KOMAİ F., HILIBAR T., SHİMİZU F., WAKEBE H.,

RA HİSHİĞAKİ H., WATBANDE T., SUÇİYAMA A., TAKAMOLO M., KAWAKAMİ B.,

RA MARAĞAYA S., KOMIYAMA H., SACON N., TAKAMİ S., PÜKUZUMİ Y.,

RAMAZAKİ M., WATBANDE T., SUĞIYAMA A., TAKAMOLO M., KAWAKAMİ B.,

RAMAZAKİ M., WATBANDE K., KUMAĞBİ A., İLAKURA S., FUKUZUMİ Y.,

RAMAZAKİ M., WATBANDE K., KUMAĞBİ A., İLAKURA S., FUKUZUMİ Y.,

RAMAZAKİ M., WATBANDE K., KUMAĞBİ A., İLAKURA S., FUKUZUMİ Y.,

RAMAZAKİ M., WATBANDE M., TASHİNOH N., TAKAMI T.,

RAMAZAKİ M., WATBANDE M., TASHİNOH N., TAKAMI T.,

RAMAZAKİ M., WATBANDE M., TASHİNOH N., TAKAMI T.,

RAMAZAKİ M., WATBANDE M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI S.,

RAWADATA Y., KOMIYAMA M., TAKAMI M., TAKAMI T.,

RAMADATA Y., KOMIYAMA M., TAKAMI S.,

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RAMADATA Y., KOMIYAMA M., TAKAMI 
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ13898.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
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                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                        Length 434;
EMBL; AL833939; CAD38794.1; -; mRNA.
EMBL; BC098298; AAH982981.1; -; mRNA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
                                                                                                           InterPro; IPR004344; Tub_tyr_ligase.
Pfam; PF03133; TTL; 1.
Hypothetical protein: SEQUENCE 434 AA; 49433 MW; 9E79E6CA08651CA1 CRC64;
                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                     65.4%; Score 850; DB 2;
61.8%; Pred. No. 9.7e-68;
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                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.8%
Matches 152; Conservative
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Q9H876;
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452
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                                                                                                                                                                                                                                                                        1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEBILBLAAADHPLSRDNKWVVQKYIETPLLICD 60
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Matanabe M., Komateu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                     TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                                                                                                                                181 YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A633053H17 product:HOTTL PROTEIN homolog.
Name=483341J24Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUB=Thymus;
MEDLINE=21085660; PubMed=11217951; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda
                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                            Length 744;
                                                                                                                                                                                                                                                   49; Indels
                                                                                                                                      activity; IEA.
                                                                                                                                                                                                       744 AA; 84683 MW; DF661753E4AFF0DF CRC64;
                                                                                                                                                                                                                             65.4%; Score 850; DB 2;
61.8%; Pred. No. 1.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     704 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                         Nat. Genet. 36:40-45(2004).

EMBL, AK023960; BAB14741.1; -; mRNA.

Ensembl; ENSG0000156983; Homo sapiens.

GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0004835; F:tubulin-tyrosine ligase ac.

GO; GO:0006464; P:protein modification; IEA.

InterPro; IPR004344; Tub_tyr_lygase.
                                                                                                                                                                                                                                                   41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBBV51 MOUSE PRELIMINARY;
Q8BV51;
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                        Pfam; PF03133; TTL; 1.
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ELIYKQ 518
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                                                                                                                                                                                                                                                    152;
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                                                                                                                                                                                                       SEQUENCE
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Adachi S., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adadachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Ankuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Anori F., Innotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Antara K., Innotani Y., Kondo S., Konno H., Kawai J., Kojima Y., Kondo S., Konno H., Kasukawa T., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazuo N., Osato N., Osato H., Saito R., Saito R., Saito R., Saito R., Saito H., Saha C., Sakai K., Sakazume N., Sano H., Agawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T., Toya T., Yasuuishi A., Muramatsu M., Hayashizaki Y., Tuya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Embl., AKO80321; BAC37878.1; -; mRNA.

Bubambi, ENSWUSGO00003276; Mus musculus.

ROJ, GO:0004885; F:tubulin-tyrosine ligase activity; IEA.
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadeta K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gasateriand T., Gissi C., King B., Kochiwa H., RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brackincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N., A Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hayshizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I is an analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length DNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Functional annotation of a full-length mouse cDNA collection.";
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SEOUENCE 704 AA; 79080 MW; 3FAD889C1DBSCF7D CRC64;
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InterPro; IPR004344; Tub_tyr_ligase.
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Board S.G., Loquelland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellando N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Norliguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                               1;
                                                                    120
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                                                                                                                         |:|| |||:| |||:|| ||| 363 HPMLPPDNMWSSQRFQAHLQEVDAPKAWSSVIVPGMKAAVIHALQTSQDNVQCRKASFEL
                                                                                                                                                                                                                                   SPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL
                                                      1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICD
                                                                                                            TKFDIROWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR
                                                                                                                                                                                                                     YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAV----DRSCDIGNF
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                               Gaps
                               4.
  Length 704;
                             49; Indels
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Ensembl; ENSMUSG0000030276; Mus musculus.
MGI: MGI:2141418; 48334417248ik.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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 ; Score 838; DB 2;
; Pred. No. 2.1e-66;
43; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                           266 AA.
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NIH MGC Project;
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64.5%;
ilarity 61.0%;
Conservative 4
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
4833441J24Rik procein.
Name-4833441J24Rik;
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Q922TO;
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NUCLEOTIDE SEQUENCE.
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               Similarity
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                           Matches 150;
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 Query Match
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Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
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Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
Casas E., Wray J.E., White J., Cho J., Pahrenkrug S.C., Bennett G.J.
Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle."; Genome Res. 11:626-630(2001).
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BT021865; AAX46712.1; -; mRNA.
Pfam; PF03133; TTL; 1. - - SEQUENCE 266 AA; 30506 MW; F8E8FB52FA8B8E98 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Tubulin tyrosine ligase-like family, member 3.
Name=TTLL3;
                                                                                                                                    49;
                                                                               Query Match 64.2%; Score 834; DB 2; Best Local Similarity 60.6%; Pred. No. 1.5e-66; Matches 149; Conservative 44; Mismatches 49;
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241 ELIYKQ 246
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SPILLPAHNWWISTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSFEL 180
GADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCD----IGNFE 237
                       1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICD 60
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ORFNames-ENSANGG0000019848;
Anopheles gambiae str. PEST.
ENATYOLA: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.

EMBL, AAABO1008980; EAA13905.2; -; Genomic_DNA.
GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA.
GO; GO:0006464; P:protein modification; IEA.
InterPro; IRR004344; Tub_tyr_lygase.
PF03133; TTL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67109 MW; 8938D9EDD5935071 CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                            572 AA.
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                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                            ANOGA PRELIMINARY;
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572 AA;
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Matches 124;
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SEQUENCE
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Q9VM91 DROME
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                                              TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQKYLKNDVGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Schachter V., Odetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
Wincker D., Lander E.S., Weissenbach J., Roest Crollius H.;
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                                                                                                                                                  2 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVQKYIETPLLICDT
      3 MEGDRNIWIVKPGAKSRGRCIMCMDHLEEMLKLVDCNPMMMKDGKWVVHNYIERPLLIFG
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;

Bukaryota, Metorerygii, Teleostei, Buteleostei, Neoteleostei,

Acanthomorpha, Acanthopterygii; Percomorpha, Tetraodontiformes;

Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                             YGADFVLGRDFRPWLIEINSSPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCD 232
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                                                                                                                                                                                                                                  Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.5%; Score 786; DB 2; Length 534; 59.2%; Pred. No. 7e-62;
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                                                                                                                                                                                                                                                                                                                                                                                         13-5EP-2005 (TrEMBLrel. 31, Created)
13-5EP-2005 (TrEMBLrel. 31, Last sequence update)
13-5EP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 11 SCAF14979, whole genome shotgun sequence.
ORFNames=GSTENG00027209001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
; CAAE01014979; CAG06724.1; -; Genomic_DNA.
ENCE 534 AA; 60130 MW; 62B5BBBB696B662B CRC64;
                                                                                                                                                                                                                                                                                                                                                        534 AA
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Nature 431:946-957(2004).
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Matches 145; Conservative
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Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
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RA MEDLINES-20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Farnas C.A., Goccayne J.D., R.A Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F., A manatides P.G., Scheer S.E., Lip P.W., Hoskins R.A., Galle R.F., A schoer S.E., Edwicker S.E., Champe M., Feiffer B.D., R. Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Baradon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Ballew B. M., Basu A., Baxendale J., Bayraktarzoglu L., Beasley E.M., Basu A., Baxendale J., Bayraktarzoglu L., Beasley E.M., Basu A., Baxendale J., Bayraktarzoglu L., Beasley E.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., R. Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P., Bortore P.W., Cauley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cauley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cauley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cauley S., Danks A.D., Berlos C.C., Ferraz C., Ferriera S., Plunkov B. C., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Plunkov B., Chan D., Harris M., L. Harris M., L. Harris M., L. Harris M., L. Harris M., Andrei B., Rodried C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitzky A.A., Heiman T.J., Hernandez J.R., Harris M., Andrei B., Molincoh T.C., Molecod M.P., McDerson D.L., Merluov G., Milshina N., Murphy B., Murphy L., Muzny D.M., Neston D.L., New Reinert K., Remigeton K., Sunders R.D., Scheeler F., Shen H., Spier E., Spradling A.C., Stapleton M., Strong R., Yen B., She B. C., Scheel F., Wolley K.C., Wu D., Yang S., Yao Q.A., Ra P., Mars Sarman D.A., Weinsteen D., Ra Reinert K., Remigeton K., Saunders R.D., Chollard W., Shue B.C., Siden-Kiamos I., Shue S., Phol. Stand M., Shue B.C., Siden-Kiamos I., Shue S., Chollar K., Wang S., Yao Q., Zhan M., Yells Shue B., Shue B., Rodrier E., Spradling A.C., Stapleton M., Velly W., Wang S., Yao Q., Zhan M., Wang S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WUCLEOTIDE SEQUENCE.
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R., Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
                                                                                           Name-CG11223, ORFNames-CG11323,
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                    Last sequence update)
Last annotation update)
 992 AA.
                                                                                                                                                                 Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                   Created)
 PRT;
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                               01-MAY-2000 (TrEMBLrel. 13,
                                               01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
Q9VM91_DROME PRELIMINARY;
Q9VM91;
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468
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MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
Anophelinae, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                             Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
                                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 992;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004835; F:tubulin-tyrosine ligase activity; IEA. GO; GO:0006464; P:protein modification; IEA. INEA. InterPro; IPR004344; Tub_tyr_lygase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan, PF03133; TTL, 1. - - SEQUENCE 992 AA; 112255 MW; 0FC34674C15BDAAD CRC64;
                                                                                                                                                                                                                                                                  systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE003614, AAF52432.1, -, Genomic DNA.
Ensembl, CG11323, Drosophila melanogaster.
Flybase, FBgn0031854; CG11323.
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01-MAR-2004 (TrEMBLrel. 26, Lus
01-MAR-2004 (TrEMBLrel. 26, Lus
BNSANGPO000022334 (Fragment)
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Q7PMD3;
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262 IDGIRNMWILKPGNRCRGLGIMLFNDDRKLLEHVDS----NPDVKYVAQKYIERPLLIHC 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TKFDIRQWFLVT-DWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAVQK-YLKNDV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 GRSPLLPAHNWWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPRKNSF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELYGADFVLGRDFRPWLIEINSSPTMHPSTPVTAQLCAQVQEDTIKVAVDRSCD----IG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEELLELAAADHPLSRDNKWVVQKYIETPLLICD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Indels 10; Gaps
                                                                                                                                                              The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/AAABO1008980; EAA13971.3; -; Genomic_DNA.
GO; GO:000464; P:protein modification; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR0434; Tub_tyr_lygase.
PR03113; TTL, 1.
PR051IE; PS50975; ATP_GRASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 501;
                                                               The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     501 501
501 AA; 58862 MW; 806539A2FD8E76DF CRC64;
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40.1%; Score 521; DB
Best Local Similarity 45.9%; Pred. No. 4.4e-
Matches 112; Conservative 41; Mismatches
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STRAIN=PEST;
                                  NUCLEOTIDE SEQUENCE
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NCBI_TaxID=180454;
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GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2006, 12:45:31; Search time 8.99628 Seconds

(without alignments)

2588.231 Million cell updates/sec
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US-10-635-977-2_COPY_133_374 1299 1 IDGLRNIWIIKPAAKSRGRDIKVAVDRSCDIGNFELLWRQ 242	BLOSUM62 Gapop 10.0 , Gapext 0.5	283416 seqs, 96216763 residues
Title: Perfect score: Sequence:	Scoring table: BLOSUM62 Gapop 10	Searched:

283416	
Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

0% 100% 45 summaries	
Match Match first	***
Minimum Maximum Listing	PIR 80:* : pir1:: pir2:: : pir3::
	 H (1) W 44
Post-processing:	Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	w	protein ZK1128.6 [hypothetical prote		o	hypothetical prote		8	hypothetical prote				ρ	progesterone recep	probable transport		probable transport	probable protein k	calmodulin-binding	DNA topoisomerase	probable RING zinc	cyclin E - Caenorh	hypothetical prote	glucosyltransferas	probable U5 snRNP-	anticodon nuclease	aldehyde dehydroge	hypothetical prote
SUMMARIES	QI	T12515	A45443	E88575	T27699	T20262	C89217	T20343	A96805	T37571	S48261	T01270	T30888	T45824	E89920	A25923	F91218	H86064	D65182	A25698	JH0588	AC1419	B84813	T43050	T30156	T30858	T39188	H81152	T04594	877908
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æ	Query	65.4	19.1	18.7	18.7	16.1	16.1	12.0	12.0	11.9	11.1	6.7	6.5	6.5	6.4	6.4	6.4	6.4		•	•	6.3		•	•	•	6.2		•	
	Score	850	247.5	243	243	209.5	209.5	156	155.5	155	144	87	82	84.5	83.5	83.5	82.5	82.5	82.5	82	æ	81.5	81	81	81	80	80	σ	79.5	6
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A4543 445443 4. Webland, J.; Plessmann, U.; Dodemont, H.; Gerke, V.; Weber, K. J. Cell Biol. 120, 735-732, 1993 4. Trosine ligase (EC 6.3.2.25) [validated] - pig C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; PErsfeld, K.; Webland, J.; Plessmann, U.; Dodemont, H.; Gerke, V.; Weber, K. J. Cell Biol. 120, 725-732, 1993

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F17F16.1 protein - flagellar biosynth flagellar biosynth hypothetical prote DNA strand transfe ribosomal protein violaxanthin de-ep probable thermosta probable anthranil hypothetical prote DNA polymerase gam hypothetical prote hypothetical ABC t large T antigen - adenylate cyclase transcription regu	ALIGNMENTS - human on 23-Jul-1999 #text_change 09-Jul-2004 .W.; Gassenhuber, J.; Wiemann, S. tabase, June 1999 UNIPARC:UD100001377A6; EMBL:AL096725 clone DKFZp434B103	### ### ### ### #### #################
D86303 A64650 E71937 F71937 F71937 G69537 G701158 T04208 T04208 A82714 A82986 AR2725	1 si ba ';	milarity 61.8%; Score 850; D Conservative 41; Mismatches Conservative 41; Mismatches DGLRNIWIIKPAAKSRGRDIVCMDRVEEILEL:
2142 733 2 733 2 742 2 286 2 286 2 286 2 286 2 285 2 1113 2 627 2	DKFZp434B103. ens (man) #sequence_revi er, D.; Mewes, tein Sequence 217524 AA AM> UNIPROT:Q9Y4R7 e: adult testi	65.4%; ative fl.8%; KPAAKSRG KPGAKSRG VTDWNPLT I VIDWNPLT ISTREQEY SQRFQAH FRPWLIEI
	S C WAY ZOTE #6	Similarity 2. Conserva 1DGLRNIMIIK SI
29.5 20.7 20.8 20.8 20.8 20.8 20.8 20.8 20.8 20.8	ical protein 18: John Sapie 23-Jul. 1999 10n: T12515 t, R.; Heubne 10 the Protein Protein Protein Protein Protein Protein Protein Protein Protein Protein Protein Protein Protein Protein RNA es: 1-352 cWA es:	atch cal Si 152; 152; 152; 1 I I I I I I I I I I I I I I I I I I
U U U U U U U U U U U U U U U U U U U	RESULT 1 T12115 hypothetical protein DKI C;Spocies: Homo sapiens C;Date: 23-Jul-1999 #sec C;Accession: T12515 K;Wambutt, R.; Heubner, submitted to the Protein A;Reference number: 2177 A;Accession: T12515 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-352 <wam>A;Residues: 1-352 <wam>A;Residues: 1-352 <wam>A;Residues: 1-352 <wam>A;Residues: 1-352 <wam>A;Rosicule type: mRNA A;Residues: 1-352 <wam>A;Roperimental source: C;Genetics: A;Note: DKFZp434B103.1</wam></wam></wam></wam></wam></wam>	Query M Best Lo Best Lo Qy Db Cy Db

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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E88575
B;Anonymous, The C. elegans Sequencing Consortium.
Socience 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: E88575
A;Accession: E88575
A;Accession: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-640 <STO>
A;Cross-references: UNIPROT:Q09647; UNIPARC:UPI000017A077; GB:chr_III; PIDN:CAA87425.1;
                                                                                                        GB:X68453; GB:S54050; NID:g21
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                                                                                                                                                                                                                                                                                                                             --CDTKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKL-DSAIHLCNNAVQKYLK 115
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                    A;Accession: A45443
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-379 <ERS>
A;Cross-references: UNIPROT:P38160; UNIPARC:UPI00001377A9; GB:X68453; GB:S;A;Experimental Bource: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:123858, NCBIP:123859)
C;Keywords: ligase
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A; Reference number: A45443; MUID:93147125; PMID:8093886
                                                                                                                                                                                                            Query Match 19.1%; Score 247.5; DB 2; Best Local Similarity 29.4%; Pred. No. 4.4e-15; Matches 69; Conservative 40; Mismatches 93;
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Matches 67; Conserv
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A) Before to the EMBL Data Library, January 1995
A; Reference number: 220407
A; A; Accession: T27699
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residuae: 1-680 < MIL.
A; Cross-references: UNIPROT: Q09647; UNIPARC: UP1000017A076; EMBL: 247357; PIDN: CAA87425.2
A; Experimental source: clone ZK1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1198 <WIL>
A;Cross-references: UNIPROT:017720; UNIPARC:UPI000017A066; EMBL:Z81051; PIDN:CAB02862.2
A;Experimental source: clone C55A6
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A;Introns: 32/3; 68/1; 107/3; 201/3; 273/1; 364/3; 407/3; 460/3; 476/2; 534/2; 677/3; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H----VEPRKNSFELYGADFVLGRDFRPWLIEINSSPIMHPSTPVTAQLCAQVQEDTIKV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 HMSRFLEQEPICYELPGIDIILDEDYKPWLLEVNISPSLHSGTPLDVSVKAPLAKDVLNL 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypochetical protein C55A6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20262
R;Kershaw, J.
R;Kershaw, J.
Rubmitted to the EMBL Data Library, October 1996
hypothetical protein ZK1128.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 KFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDK---LDSAIHLCNNAVQKYLKND-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: CSSP: ZK1128.6
A;Map position: 3
A;Introns: 114/1; 208/3; 242/3; 334/3; 362/2; 405/2; 424/2; 550/2; 633/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.7%; Score 243; DB 2; Length 680; 27.8%; Pred. No. 2.5e-14; ive 47; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: T20262
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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11;

42;

Length 662; Indels 28

113

169

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A;Cross-references: UNIPARC:UPI000013B847; EMBL:Z47809; PIDN:CAA87783.1; GSPDB:GN00020 A;Experimental source: clone F42A8 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.0%; Score 156; DB 2; Best Local Similarity 25.8%; Pred. No. 2.7e-06; Matches 62; Conservative 36; Mismatches 100
                                                                                                    A,Reference number: 219510
A,Accession: T22085
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-662 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
A;Introns: 78/2; 114/3; 330/3; 471/1; 521/2; 587/2
                                                                           Data Library, January 1995
   A;Experimental source: clone D2013 R;Matthews, P. submitted to the EMBL Data Library,
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Best Local Similarity 25.39
Matches 55; Conservative
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A;Molecule type: DNA
A;Residues: 1-883 <STO>
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A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A,Accession: C89217
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A;Cross-references: UNIPROT:Q09512; UNIPARC:UP1000013B847; EMBL:Z47808; PIDN:CAA87778.1;
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د.ئـ
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                                                                       764
                                                                                                                                 68 WFLVTDWNPLTIWFYKESYLRPSTQRF--SLDKLDS--AIHLCNNAVQK----YLKNDVG 119
                                                                                                                                                                                                                                                                         120 RSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKAIAHAMKVAQDHV--EPRKN- 176
                                                                                                                                                                                                                                                                                                                 : || : || : || : || 3.4 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5 || 3.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein D2013.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T20343; T22085
R;Mortimore, B.
submitted to the EMBL Data Library, January 1995
A;Reference number: Z19259
A;Accession: T20343
A;Accession: T20343
A;Accession: Pealiminary; translated from GB/EMBL/DDBJ
A;Reference number: DNA
                                       WIIKPAAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTKFDIRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          880 RFACTNFELFGFDVLVDQALKPWLLEVNLSPSLACDAPLDSLLKTRLIADLLNLA 934
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Best Local Similarity 25.5%
Matches 60; Conservative
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A; Residues: 1-1203 <STO>
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A;Map position: 5
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hypothetical protein T5M16.14 [imported] - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: Aspecies: A
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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A;Accession: 845962
A;Molecule type: DNA
A;Residues: 1-753 <FEB.
A;Residues: 1-753 <FEB.
A;Cross-references: UNIPARC:UP1000013A3DD; EMBL:Z35963; NID:G536366; PIDN:CAA85047.1; P:R;Dekker, P.J.T.; Hoekert, W.; van Oosterum, K.; Grivell, L.A.
submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 167-351, TPE', 356-449, 'A', 451-562, 'R', 564-753 <DEK>
A;Cross-references: UNIPARC:UP10000168D37; EMBL:X69881; NID:g4086; PIDN:CAA49508.1; PID
C;Genetics:
A;Cross-references: SGD:S0000298
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Nylternate names: hypothetical protein F27F23.2; hypothetical protein T20K24.23
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Peb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01270; T00543; Ā84574
C;Accession: T01270; T00543; Ā84574
Simponsley, S.D. Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau submitted to the EMBL Data Library, May 1998
A;Pescription: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence.
A;Reference number: Z14177
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A/Status: translated from GB/EMBL/DDBJ
A/Status: translated from GB/EMBL/DDBJ
A/Status: 1-439 «RODA
A/Residues: 1-439 «RODA
A/Residues: 1-439 «RODA
A/Cross-references: UNIPROT: O65915; UNIPARC: UPI00000A9775; EMBL. AC003058; NID: 93135250;
A/FEXPERIMENTAL SOURCE: cultivar Columbia
R/Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, Embnitted to the EMBL Data Library, July 1997
A/Pescription: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A/Reference number: Z14167
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y., M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
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A;Accession: S41800
A;Reference number: S45927
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Matches 57; Conserve
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A; Residues: 1-439 <ROW>
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A; Residues: 1-753 <MAN>
A; Cross-references: UNIPROT: P38254; UNIPARC: UPI000013A3DD; EMBL: X78993; NID: 9476045; PID
R; Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tubulin-tyrosine ligase related protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Cacssion: T3751
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z21726
A;Accession: T37571
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Wolecule type: DNA
A;Residues: 1-403 - GABD>
A;Cacss-references: UNIPROT:Q10438; UNIPARC:UP1000013A94B; EMBL:Z70721; PIDN:CAA94694.1;
A;Experimental source: strain 972h-; cosmid c12B10
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                                                                                                                          144 YILKPSMCDRAQGIRLFSTIEELQAIFDSFDDEESESEEAGLEEKGDITVAFNNKIVISQ 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | : | : | : | : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                             --IYPSMK---KAIAHAMK 165
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NyAlternate names: hypothetical protein YBR0821
C;Species: Saccharomyces cerevisian
C;Species: Ol-Mug-1995 #sequence revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: $48261; $45962; $41800; $44676
R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Reference number: $48255; MUID:95208357; PMID:7900426
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                                                                                                                                                                                                                                                                                                                                               VAQDHVEPRKNSFELYGADFVLGRDFRPWLIEINSSP 202
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A,Status: nucleic acid sequence not shown
                                                             PLLPAHNMWTSTRFQEYLQRQG--
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Best Local Similarity 21.3%;
Matches 54; Conservative 5
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A;Gene: SPDB:SPAC12B10.04
A;Map position: 1
A;Introns: 320/3; 348/3
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Zipp, M.; Mewes, H.W.; Lemcke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B89920
B;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ca; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, J.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MUD:21311952; PMID:11418146
A;Retension: E89920
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <KUR>
        1289 GAVFQGKNKAEYAATFAMANSPVDPKSRVVFYYGSNPAQQKNYQICL----SAQSSRPKV 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 FDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKL-------DSAIHLCNNAV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 QKYLKNDVG------RSPLLPAHNMWTSTRFQEY--LQRQGRGAVWGS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appothetical protein F2K15.50 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: T8624
R.FRieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H. Strieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H. Submitted to the Protein Sequence Database, January 2000
A;Recension: T45824
A;Status: preliminary
A;Molecule type: DABA
A;Residues: 1-522 - KIE>
A;Cross-references: UNIPROT:Q9M3B3; UNIPARC:UPI000000C655; EMBL:AL132956
A;Experimental source: cultivar Columbia; BAC clone F2K15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 TPİKGDFLST-----KSKOLRLVHRTVSLDDİKLTKNAMMMTINDVVLGVTQAĞL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 RNIWIIKP--AAKSRGRDIVCMDRVEEILELAAADHPLSRDNKWVVQKYIETPLLICDTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.5%; Score 84.5; DB 2; Length 522; Best Local Similarity 21.8%; Pred. No. 8.1; ... Matches 48; Conservative 31; Mismatches 62; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ----VIYP---SMKKAIAHAMKVAQDHVEPRKNSFELYGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 3
A;Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3
A;Note: FZK15.50
                                                                                                                  1374
                                                                PVTAQLCAQVQEDTIKVAVD----RSCDIG
                                                                                                                  1345 PVMDFIKALKADPTTKFAADLKFGEQCQSG
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C;Species: Athalia rosae
C;Species: Athalia rosae
C;Species: Athalia rosae
C;Species: Athalia rosae
C;Species: Athalia rosae
C;Species: O2-Sp-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T3088
R;Nose, Y: Lee, U; Ueno, T.; Hatakeyama, M.; Oishi, K.
Insect Biochem. Mol. Biol. 27, 1047-1056, 1997
A;Title: Cloning of cDNA for vitellogenin of the parasitoid wasp, Pimpla nipponica (Hyme A;Reference number: Z20922; MUID:98231104; PMID:9569645
A;Reference number: Z20922; MUID:98231104; PMID:9569645
A;Residue: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residue: 1-1872 cNOS>
A;Residues: 1-1872 cNOS>
A;Cross-references: UNIPROT:Q17083; UNIPARC:UPI0000083E90; EMBL:AB007850; NID:d1170514;
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                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 HLFTKESWKMILEKINRITGLGYTHKQLENHFTRTRTSWK-----HWCETIASPIMKWD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 VGRSPLLPAHNMWTSTRFQEYLQRQGRGAVWGSVIYPSMKKALAHAMKVA---QDHVEPR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 ANTRKFGATEEDW-----DKYLMINKRARVF------KRRHIPHADKLATIFKGRIEPG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNSFELYGADFVLGRDFRPWLIEINS-SPTWHPSTPVTAQLCAQVQEDTIKVAVDRSCDI 233
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                      DB 2; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                        22 VCMDRVEE----ILELAAADHPLSRDNKWVVQKYIETPLLICDTKFD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 TDWNPLTIWFYKESYLRFSTQRFSLDKLDSAIHLCNNAV------
                                                                                                                                                                                                                                                                                                                                                        96; Indels
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A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: A84574
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                                                                                                                                                                                                                                                                                             Query Match
6.7%; Score 87; DB 2
Best Local Similarity 23.4%; Pred. No. 3.8;
Matches 57; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: Vg
C;Superfamily: boll weevil vitellogenin
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88 RFSTORFSLDKLDSAI----HLCNNAVOKYLKNDVGRSPLLPAHNNWTSTRFOEYLORQ 142
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                                               200
                                                          KESYLRFSTORFSLDKLDSAIHLCN-NAVOKYLKNDVGRSPLLPAHNMWTSTRFQEYLOR 141
                                                                                                                                                                              progesterone receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
                                               142 QGRGAVWGSVIYPSMKKAIAHAMKVAQDHVEPR-KNSFELYGADFVLGRDFRPWLIEINS
                                                                                                                                                                                                                                                                                                                                                                                                                           45; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
6.4%; Score 83.5; DB 2; Length 930;
Best Local Similarity 26.0%; Pred. No. 21;
Matches 33; Conservative 20; Mismatches 45; Indels 25
                                                                                                           201 SP----TMHPSTPVTAQLCAQVQEDTIKVAVDRSCDIGN 235
               Search completed: April 4, 2006, 12:51:55 Job time : 10.9963 secs
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380 QPPALKI 386
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